

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2002, 11:10:46 ; Search time 3842.15 Seconds
(without alignments)
1794.782 Million cell updates/sec

Title: US-09-394-745-6886
Perfect score: 418
Sequence: 1 agagaggggaggggtcggcgca.....tgtctacctgcgccaacttt 418

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*

28: em_un:*
 29: em_vi:*
 30: em_htgo_hum:*
 31: em_htgo_inv:*
 32: em_htgo_rod:*
 33: em_htg_hum:*
 34: em_htg_inv:*
 35: em_htg_rod:*
 36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Query Match Length DB	ID			
	1	94	22.5	1118	8	AF232008	AF232008 Zea mays
	2	85.8	20.5	1091	8	HVU43497	U43497 Hordeum vul
	3	81.8	19.6	1563	8	AB012103	AB012103 Triticum
	4	68.6	16.4	545	8	AF285163	AF285163 Oryza sat
	5	67	16.0	631	8	OSAF001395	AF001395 Oryza sat
	6	65.4	15.6	724	8	S45168	S45168 salT=15 kda
	7	64.8	15.5	623	8	HVU237754	AJ237754 Hordeum v
	8	61.8	14.8	1209	8	TAU32427	U32427 Triticum ae
	9	61.8	14.8	1250	6	AR016814	AR016814 Sequence
	10	61.8	14.8	1250	6	AR020840	AR020840 Sequence
	11	61.8	14.8	1250	6	AR027163	AR027163 Sequence
	12	61.8	14.8	1250	6	AR038450	AR038450 Sequence
	13	61.8	14.8	1250	6	AR064592	AR064592 Sequence
	14	61.8	14.8	1250	6	AR067517	AR067517 Sequence
	15	61.8	14.8	1250	6	I38469	I38469 Sequence 39
	16	61.8	14.8	1250	6	I56944	I56944 Sequence 39
	17	61.8	14.8	1250	6	I59810	I59810 Sequence 39
	18	61.8	14.8	1250	6	I75137	I75137 Sequence 39
	19	56	13.4	457	11	G71368	G71368 VE0061311FM
	20	53	12.7	89172	8	AC084295	AC084295 Oryza sat
c	21	53	12.7	169441	2	AC091787	AC091787 Oryza sat
	22	50.2	12.0	1792	8	AF021258	AF021258 Hordeum v
	23	47.4	11.3	1505	8	HVU43496	U43496 Hordeum vul
	24	47.4	11.3	3786	8	AF021256	AF021256 Hordeum v
	25	45.8	11.0	4487	8	AF021257	AF021257 Hordeum v
	26	42.4	10.1	3350	8	OSGOS9G	X51909 O. sativa (
	27	42.4	10.1	63489	8	AP002864	AP002864 Oryza sat
	28	41.6	10.0	362	8	RIC335GS9	D10956 Rice mRNA f
	29	41.6	10.0	552	8	AF064032	AF064032 Helianthu
	30	41.6	10.0	829	8	AF064030	AF064030 Helianthu
	31	41.6	10.0	15348	1	AE007163	AE007163 Mycobacte
	32	41.6	10.0	47852	1	MTV023	AL022022 Mycobacte
	33	41	9.8	675	8	AF064031	AF064031 Helianthu
	34	40.6	9.7	139487	2	AP003513	AP003513 Oryza sat
	35	39.8	9.5	1111	1	MSGRS	M95490 Mycobacteri
	36	39.6	9.5	1139	8	AB012605	AB012605 Oryza sat
	37	39.6	9.5	120593	8	AP002870	AP002870 Oryza sat
	38	39.6	9.5	144340	8	AP003852	AP003852 Oryza sat

	39	39.2	9.4	12776	1	AE004627	AE004627 Pseudomon
	40	38.6	9.2	329709	1	AP002997	AP002997 Mesorhizo
	41	38.4	9.2	44109	1	SC5F1	AL450165 Streptomy
c	42	38	9.1	1162	6	AR016817	AR016817 Sequence
c	43	38	9.1	1162	6	AR020843	AR020843 Sequence
c	44	38	9.1	1162	6	AR027166	AR027166 Sequence
c	45	38	9.1	1162	6	AR038453	AR038453 Sequence

ALIGNMENTS

RESULT 1

AF232008

LOCUS AF232008 1118 bp mRNA PLN 24-JUL-2000

DEFINITION Zea mays beta-glucosidase aggregating factor precursor, mRNA, complete cds.

ACCESSION AF232008

VERSION AF232008.2 GI:9313026

KEYWORDS .

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 1118)

AUTHORS Esen, A. and Blanchard, D.J.

TITLE A specific beta-glucosidase-aggregating factor is responsible for the beta-glucosidase null phenotype in maize

JOURNAL Plant Physiol. 122 (2), 563-572 (2000)

MEDLINE 20144023

PUBMED 10677449

REFERENCE 2 (bases 1 to 1118)

AUTHORS Blanchard, D. and Esen, A.

TITLE Cloning and sequencing of a cDNA coding for a beta-glucosidase aggregating factor (BGAF) from maize (Accession No. AF232008) (PGR 00-44)

JOURNAL Plant Physiol. 122 (3), 985-986 (2000)

REFERENCE 3 (bases 1 to 1118)

AUTHORS Blanchard, D.J. and Esen, A.

TITLE Direct Submission

JOURNAL Submitted (07-FEB-2000) Biology, Virginia Tech, 2119 Derring Hall, Blacksburg, VA 24061-0406, USA

REFERENCE 4 (bases 1 to 1118)

AUTHORS Blanchard, D.J. and Esen, A.

TITLE Direct Submission

JOURNAL Submitted (21-JUL-2000) Biology, Virginia Tech, 2119 Derring Hall, Blacksburg, VA 24061-0406, USA

REMARK Sequence update by submitter

COMMENT On Jul 21, 2000 this sequence version replaced gi:7960212.

FEATURES Location/Qualifiers

source 1..1118

/organism="Zea mays"

/db_xref="taxon:4577"

CDS 44..964

/note="heat-shock protein (Hsp); BGAF"

/codon_start=1

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/product="beta-glucosidase aggregating factor precursor"
/protein_id="AAF71261.2"
/db_xref="GI:9313027"
/translation="MASLQVTPTSAFTQWNEFKFEGLYLFHNYVGSGANQTQVISNKA
PIGIGATVVNNWTVCDGPGPNAKLIARAQGLHIQAGNWNSFSLVFVDQRFSGSTLEV
TGIVVESGEWAIVGGTGQFAMANGVISKKLHGKTSEGDIIQLTIHAFCPVLGATKRSA
TKVGPWGGSGGSPMDITAEPQRLKSITVATGIAVTSIAFSYVDSAGQTQSAGRWGGSG
GETEPVIQLGDSEVLTELSGTIGNVDGLTVITSIKFVTSKTYGPFPAWNGSDTPFA
IPVQQGSAIVGFFARAGVYLDALGVYVRSL"
mat_peptide 158. .961
/product="beta-glucosidase aggregating factor"
BASE COUNT 239 a 320 c 318 g 241 t
ORIGIN

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Query Match          22.5%;  Score 94;  DB 8;  Length 1118;
Best Local Similarity 57.0%;  Pred. No. 5.3e-10;
Matches 213;  Conservative 0;  Mismatches 152;  Indels 9;  Gaps 2;

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Qy      25 atcgcaacaacggagccgcgagggcgctctgcaaaacctgaccgtccgccccggcggttgcc 84
      || | | | ||||      |||  ||||| | | | | |||||      | ||| | |||
Db      563 ATGGACATCACGGCAGAGCCCCAGCGTCTGAAGAGCATCACCGTTGCTACTGGCATCGCC 622

Qy      85 gtggactccatcgagttcacctacaccgacacaggtggccagacgcgcaccgctggggcga 144
      |||  ||| || | | ||| |||||  |||| | | ||||| || | | ||||| ||
Db      623 GTGACCTCGATTGCCTTCTCCTACGTCGACTCCGCCGGCCAAACCCAATCTGCTGGTTCGC 682

Qy     145 tgggggtgg---acttggcggaacgtccggaagctcgatcttggcgacgctgaatacgtc 201
      ||||| ||      ||| | | | | | | | | | | | | | | | | | | |
Db      683 TGGGGCGGTTCCGGTGGAGAACTGAGCCGGTGATCCAGCTCGGTGACTCCGAGGTGCTC 742

Qy     202 aaggaagtttctggaacgtacggcgcatcgaaggtgcgactaccctgacctcggttgagg 261
      | ||| | | | | | | | | ||||  |||| | | | | | | | | | | | |
Db      743 ACGGAGCTGTCCGGGACGATCGGCAACGTCGACGGCCTCACCGTCATAACCTCCATCAAG 802

Qy     262 attgtcaccagc-----accgccagagcttggggggccatggggcatcnagagcgggaca 315
      | ||||| |||      ||| | | ||| || ||||| | | ||| | ||
Db      803 TTCGTCACAAGCCTCAAGACCTACGGGCCTTTCGGAGCATGGGGGAACGGGAGTGACACT 862

Qy     316 cgtttctgcatcanccggcaccatcggcagcagcatcgtgggattctatggacgcgcgacg 375
      | |||  ||| ||      || ||  ||||| || |||| | ||| || |
Db      863 CCATTGCGGATCCCCGTGCAGCAAGGGAGTGCCATCGTCGGCTTCTTCGCACGAGCTGGG 922

Qy     376 aacaggctcgtcgc 389
      |  |||| |||
Db      923 GTCTACCTCGACGC 936

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```

RESULT 2
HVU43497
LOCUS HVU43497 1091 bp mRNA PLN 09-FEB-1996
DEFINITION Hordeum vulgare putative 32.7 kDa jasmonate-induced protein mRNA,
complete cds.
ACCESSION U43497
VERSION U43497.1 GI:1167954
KEYWORDS .
SOURCE barley.

```

ORGANISM *Hordeum vulgare*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; *Hordeum*.

REFERENCE 1 (bases 1 to 1091)
 AUTHORS Lee, J.E., Parthier, B. and Loebler, M.
 TITLE Jasmonate signalling can be uncoupled from ABA signalling in
 barley: Identification of jasmonate-regulated transcripts which are
 not induced by ABA
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1091)
 AUTHORS Lee, J.E.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-1995) Justin E. Lee, Hormonforschung, Institut
 fuer Pflanzenbiochemie, Weinberg 3, Halle, D-06120, Germany

FEATURES
 source Location/Qualifiers
 1. .1091
 /organism="Hordeum vulgare"
 /strain="Salome"
 /db_xref="taxon:4513"
 /clone="pJRG1c34"
 /clone_lib="gt10 cDNA library of mRNA isolated from
 jasmonate-treated barley leaves"
 /tissue_type="leaf"
 /dev_stage="7 day-old seedling"

CDS
 39. .953
 /codon_start=1
 /product="putative 32.7 kDa jasmonate-induced protein"
 /protein_id="AAA87042.1"
 /db_xref="GI:1167955"
 /translation="MATFQITPCAAFEITELNFSNLYLFHTSLGSNQNSVVIIDSNA
 TTGLGSTVVNNWSICDGSPDATVVARAQGLHIYAGNWQNTFSITFEIERFKGSTLQV
 MGISVEEGEWAIVGGTGQFAMANGVIHKKLHEQSRDGNIIELTIHGFCPVLKSESLT
 KLGPWGGNGGGDKDILEAVPRRLESITVSSGSIVDSIKFSYVDQTGQKHNA GPWGGSG
 GNQNTFVLGASEFMKEVSGTFGIYDKDRHNIITSLKFITNVKTYGPFGEAKGTPFTIP
 AQKNSSIVGFFGRSGIYLDALGVYVRPL"

polyA_signal 1071. .1076
 polyA_site 1091
 /note="18 A nucleotides"

BASE COUNT 298 a 235 c 263 g 295 t
 ORIGIN

Query Match 20.5%; Score 85.8; DB 8; Length 1091;
 Best Local Similarity 55.1%; Pred. No. 2.7e-08;
 Matches 209; Conservative 0; Mismatches 164; Indels 6; Gaps 2;

```

Qy      43 ccgaggcgtctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcgagttc 102
      || ||||| || | | | | | | | | | | | | | | | | | | | | | |
Db      576 CCAAGGCGTCTGGAGAGCATCACTGTTAGCAGCGGCTCAATTGTTGATTCAATCAAATTT 635

Qy     103 acctacaccgacacaggtggccagacgcgcaccgctgggcatgggggtggacttggcggc 162
      | || | || | || | || | || | || | || | || | || | || | || |
Db      636 TCTTATGTTGACCAGACTGGACAGAAGCACACGCTGGACCCTGGGGAGGTTCGGGAGGA 695

Qy     163 aacgtccggaagctcgatcttggcgacgctgaatacgtcaaggaagtttctggaacgtac 222
      || | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 696 AATCAAAACACGTTTGTGCTCGGCGCTTCTGAATTTATGAAGGAAGTTTCTGGAACATTC 755
 Qy 223 ggcgcacat---tcgaagggtgcgactaccctgacctcggtgaggattgtcaccagcaccgcc 279
 ||| | | ||| | | | | | | | | | |
 Db 756 GGCATTTATGACAAAGACCGACACAACATAATAACTTCCTTGAAATTTATCACGAATGTG 815
 Qy 280 agagcttggggggccatggggcatcnagagcgggacacgtttctgcatcancggcaccatc 339
 | | | |||| | | | | | | | | | |
 Db 816 AAGACGTACGGGCCTTTTCGGAGAAGCGAAGGGAACCCCTTTCACCATACCCGCGCAGAAG 875
 Qy 340 ggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgtcgctgcgatcggt 399
 ||||| |||| | | | | | | | | | |
 Db 876 AATAGCAGCATCGTTGGGTTCTTCGGGCG---TAGCGGTATATATCTTGATGCGCTTGGT 932
 Qy 400 gtctacctgcgccaacttt 418
 ||||| ||||| ||| |
 Db 933 GTCTACGTGCGCCCACTCT 951

RESULT 3

AB012103

LOCUS AB012103 1563 bp mRNA PLN 01-DEC-1999

DEFINITION Triticum aestivum mRNA for VER2, complete cds.

ACCESSION AB012103

VERSION AB012103.2 GI:6469039

KEYWORDS ver2; ver203; VER2.

SOURCE Triticum aestivum (cultivar:Jingdong No.1) seedling embryobud cDNA to mRNA.

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

REFERENCE 1 (sites)

AUTHORS Kong,K., Tan,K.H., Huang,H.L. and Liang,H.G.

TITLE Molecular cloning of a cDNA related to vernalization (ver203) in winter wheat

JOURNAL Science in China 38, 799-806 (1995)

REFERENCE 2 (sites)

AUTHORS Chong,K., Tan,K., Huang,H. and Liang,H.

TITLE Sequence analysis of vernalization-related cDNA clone from winter wheat

JOURNAL Acta Phytophysiological Sinica 23, 99-102 (1997)

REFERENCE 3 (sites)

AUTHORS Chong,K., Bao,S., Xu,T., Tan,K., Liang,T., Zeng,J., Huang,H., Xu,J. and Xu,Z.

TITLE Functional analysis of the ver gene using antisense transgenic wheat

JOURNAL Physiol. Plantarum 102, 87-92 (1998)

REFERENCE 4 (bases 1 to 1563)

AUTHORS Yong,W., Chong,K., Xu,Z., Tan,K. and Zhu,Z.

TITLE Direct Submission

JOURNAL Submitted (08-MAR-1998) to the DDBJ/EMBL/GenBank databases. Kang Chong, Chinese Academy of Sciences, Institute of Botany; Xiangshan, Beijing, Beijing 100093, China (E-mail:chongk@public.east.cn.net, Tel:86-10-82594821, Fax:86-10-82594821)

COMMENT On Nov 26, 1999 this sequence version replaced gi:3551159. Sequence updated (07-Oct-1999).

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FEATURES             Location/Qualifiers
     source            1. .1563
                        /organism="Triticum aestivum"
                        /cultivar="Jingdong No.1"
                        /db_xref="taxon:4565"
                        /dev_stage="seedling"
                        /tissue_type="embryobud"
     gene              193. .1314
                        /gene="ver2"
     CDS                193. .1314
                        /gene="ver2"
                        /note="gene expression should be induced by cold treatment
                        for 21 days in wheat and 14 days in Arabidopsis, it can
                        control initiation of flowering and development of
                        flower.; vernalization related gene"
                        /codon_start=1
                        /product="VER2"
                        /protein_id="BAA32786.2"
                        /db_xref="GI:6469040"
                        /translation="MIITNAARGRTRDIYGSTVVTTCCHSPSTASFQRTLLLPSETAR
                        MLPVSDHDSLQTGVLKSLRTLPTSPSHSPMAKFQITPFPGLVENTEFNFGSLYLYNIS
                        NPPSYASIKENNATTGWGGASLVNWQIYDGDGSGANLVGHAQGMQIHAGASHQSFTLV
                        FENGFRFGSTLYVVGQTVRVEQAGEWSIVGGTGDLMARGVVVKVFHEKVKDGNTWEL
                        RFHGFCSMQSLPTLTKTGPWGGHGGSVTESEQPWRIESMTIVHEGIIAMFSCSYVDLS
                        GKRRTTGSWGGGNGIRTKVELGPREILKAVSGTYVSLYNGQTVIESLKFVTNEGTYGP
                        YGRTTGTPFNADVPKDRSIVGFFGRADDTQLIAFGVYTV"
     polyA_site         1544
BASE COUNT            412 a      358 c      407 g      386 t
ORIGIN

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Query Match 19.6%; Score 81.8; DB 8; Length 1563;
 Best Local Similarity 50.7%; Pred. No. 1.7e-07;
 Matches 194; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

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Qy      35 cggagccgcccaggcgctctgcaaaacctgaccgtccgccccggcgcttgccgtggactcca 94
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      935 CAGAACAACCATGGCGCATAGAGAGTATGACAATCGTCCATGAGGGGATAATTGCAATGT 994

Qy      95 tcgagttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatgggggtggac 154
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      995 TTTCATGCAGTTACGTTGACCTATCTGGCAAGAGGCGCACACAGGTTCTTGGGGTGGTG 1054

Qy     155 ttggcggcaacgtccggaagctcgatcttggcgacgctgaatacgtcaaggaagtttctg 214
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1055 GTAATGGCATCCGCACAAAGGTTGAGCTGGGGCCTCGGGAGATTTTAAAAGCAGTGTCTG 1114

Qy     215 gaacgtacggcgcatcgaaggtgcgactaccctgacctcgttgaggattgtcaccagca 274
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1115 GAACATATGTCTAGCCTTTACAATGGGCAGACTGTTATTGAGTCACTTAAGTTTGTACCA 1174

Qy     275 ccgccagagcttggggggccatgggggcatcnagagcgggacacgttttctgcatcanoggca 334
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1175 ACGAAGGAACGTACGGACCATATGGCCGTACAACCGGTACACCTTTCAACGCTGACGTGC 1234

Qy     335 ccacgcgcagcagcatcgctgggattctatggacgcgcgcgaacaggctcgctcgctgcga 394
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 1235 CGAAAGACCGAAGCATCGTCGGGTTCTTTGGGCGTGCCGATGATACGCAGCTCATCGCAT 1294

Qy 395 tcggtgtctacctgcgccaactt 417

| | | | | | | | | | | | | |

Db 1295 TTGGTGTTTACACGGTCTGAATT 1317

RESULT 4

AF285163

LOCUS AF285163 545 bp mRNA PLN 02-AUG-2001

DEFINITION Oryza sativa subsp. japonica salt-induced protein mRNA, complete cds.

ACCESSION AF285163

VERSION AF285163.1 GI:15076930

KEYWORDS .

SOURCE Oryza sativa subsp. japonica.

ORGANISM Oryza sativa subsp. japonica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 545)

AUTHORS Lee, R.H. and Chen, S.C.G.

TITLE Rice cDNA encoding salt-induced protein homolog is associated with dark-induced leaf senescence

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 545)

AUTHORS Lee, R.H. and Chen, S.C.G.

TITLE Direct Submission

JOURNAL Submitted (06-JUL-2000) Institute of Botany, Academia Sinica, Taipei 11529, Taiwan

FEATURES Location/Qualifiers

source 1. .545

/organism="Oryza sativa subsp. japonica"

/cultivar="Tainong 67"

/sub_species="japonica"

/db_xref="taxon:39947"

/clone="Osl43"

/tissue_type="leaf"

/dev_stage="seedling"

CDS 41. .478

/note="dark-induced leaf senescence-associated gene"

/codon_start=1

/product="salt-induced protein"

/protein_id="AAK82986.1"

/db_xref="GI:15076931"

/translation="MTLVKIGPWGGNGGSAQDISVPPKLLGVTIYSSDAIRSI AFNY

IGVDGQEY AIGPWGGEGTSTEIKLGSSEIQIKEISGTHGPVYDLADIVTYLKI VTSAN

NTYEAGVPNGKEFSIPLQDSGHVVGFFGRSGTLIDAIGIYVHP"

BASE COUNT 149 a 121 c 139 g 136 t

ORIGIN

Query Match 16.4%; Score 68.6; DB 8; Length 545;

Best Local Similarity 51.3%; Pred. No. 0.00013;

Matches 211; Conservative 0; Mismatches 191; Indels 9; Gaps 2;

Qy 2 gagagggagggtcggcgcaggacatcgcaacaacggagccgccgaggcgtctgcaaaacc 61


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      || | ||||| || ||||| | | | | | | | | | |
Db      72 GAAATGGAGGGTCAGCTCAGGACATC-----AGTGTGCCACCCAAGAAGCTGTTAGGCG 125

Qy      62 tgaccgtccgccccggcgttgccgtggactccatcgagttcacctacaccgacacaggtg 121
      ||| | | | | | | | | | | | | | | | | | | |
Db      126 TGACAATCTACAGCTCAGATGCAATCAGATCCATTGCCTTCAACTACATCGGTGTGGATG 185

Qy      122 gccagacgcgcaccgctgggcgatggggtggacttggcggcaacgtccggaagctcgatc 181
      | || | | | | | | | | | | | | | | | | | | |
Db      186 GACAGGAATATGCCATTGGTCCATGGGGTGGGGGCGAAGGCACCTCTACAGAGATTAAAC 245

Qy      182 ttggcgacgctgaatacgtcaaggaagtttctggaacgtacggcgcatcgaaggtgcga 241
      | || | | | | | | | | | | | | | | | | | | |
Db      246 TGGGCTCCTCTGAGCAGATCAAGGAGATTTCTGGAACCCATGGCCCAGTCTATGATCTGG 305

Qy      242 ctaccctgacctcggttgaggattgtcaccagcaccgccagagcttggggggccatggggca 301
      || | | | | | | | | | | | | | | | | | | |
Db      306 CTGACATTGTACCTATCTTAAGATTGTGACAAGTGCTAATAATACATACGAGGCTGGAG 365

Qy      302 tcnagagcgggacacgtttotgcatcanccggcaccatcggcagcagcatcgtgggattct 361
      || | | | | | | | | | | | | | | | | | | |
Db      366 TCCCAAATGGAAAGGAATTTCAGATTCCACTGCAAGACTCTGGCCATGTCGTTGGATTCT 425

Qy      362 atggacgcgcgacgaacaggctcgctcgctgcgatcggtgtctacctgcgcc 412
      |||| | | | | | | | | | | | | | | | |
Db      426 TTGGAAG---GTCTGGAACGCTTATCGACGCAATTGGCATCTACGTCCACC 473

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RESULT      5
OSAF001395
LOCUS       OSAF001395      631 bp      mRNA                      PLN      06-MAY-1997
DEFINITION  Oryza sativa salt mRNA, complete cds.
ACCESSION  AF001395
VERSION    AF001395.1  GI:2072552
KEYWORDS   .
SOURCE     Oryza sativa.
  ORGANISM Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1  (bases 1 to 631)
  AUTHORS  Lee,J.S., Lee,M.C. and Eun,M.Y.
  TITLE    Identification of salt-stress induced gene from rice by
            differential display
  JOURNAL  Unpublished
REFERENCE  2  (bases 1 to 631)
  AUTHORS  Lee,J.S., Lee,M.C. and Eun,M.Y.
  TITLE    Direct Submission
  JOURNAL  Submitted (28-APR-1997) Dept. of Cytogenetics, National Institute
            of Agricultural Science and Technology, RDA, Seo-Dun Dong, Suwon
            441-707, Korea
FEATURES   Location/Qualifiers
    source  1. .631
            /organism="Oryza sativa"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="pSF4-1"

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/tissue_type="leaf"
/dev_stage="3 weeks old"
/note="1% NaCl treated"
gene      39. .476
          /gene="salt"
CDS       39. .476
          /gene="salt"
          /codon_start=1
          /protein_id="AAB53810.1"
          /db_xref="GI:2072553"
          /translation="MTLVKIGPWGGNGGSAQDISVPPKKLLGVTIYSSDAIRSI AFNY
          IGVDGQEYAIGPWGGGESTSTEIKLGSSEIQIKEISGTHGPVYDLADIVTYLKIVTSAN
          NTYEAGVPNGKEFSIPLQDSGHVVGFFGRSGTLIDAIGIYVHP"
BASE COUNT      182 a      139 c      154 g      156 t
ORIGIN

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Query Match      16.0%; Score 67; DB 8; Length 631;
Best Local Similarity 51.1%; Pred. No. 0.00027;
Matches 210; Conservative 0; Mismatches 192; Indels 9; Gaps 2;

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Qy      2 gagagggaggggtcggcgcaggacatcgcaacaacggagccgagggcgtctgcaaaacc 61
      ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| |||
Db      70 GAAATGGAGGGTCAGCTCAGGACATC-----AGTGTGCCACCCAAGAAGCTGTTAGGCG 123

Qy      62 tgaccgtccgccccggcggttgccgtggactccatcgagttcacctacaccgacacaggtg 121
      |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      124 TGACAATCTACAGCTCAGATGCAATCAGATCCATTGCCTTCAACTACATCGGTGTGGATG 183

Qy      122 gccagacgcgcaccgctgggcgatggggtggacttggcgggcaacgtccggaagctcgatc 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      184 GACAGGAATATGCCATTGGTCCATGGGGTGGGGGCGAAAGCACCTCTACAGAGATTAAAC 243

Qy      182 ttggcgacgctgaatacgtcaaggaagtttctggaacgtacggcgcatcgaaggtgcga 241
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      244 TGGGCTCCTCTGAGCAGATCAAGGAGATTTCTGGAACCCATGGCCCAGTCTATGATCTGG 303

Qy      242 ctaccctgacctcggttgaggattgtcaccagcaccgccagagcttggggggccatgggggca 301
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      304 CTGACATTGTACCTATCTTAAGATTGTGACAAGTGCTAATAATACATACGAGGCTGGAG 363

Qy      302 tcnagagcgggacacggtttctgcatcancggcaccatcggcagcagcatcgtgggattct 361
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      364 TCCCAAATGGAAGGAATTTCAGCATTCCTACTGCAAGACTCTGGCCATGTCGTTGGATTCT 423

Qy      362 atggacgcgcgacgaacaggctcgtcgctgcgatcgggtgtctacctgcgcc 412
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Db      424 TTGGAAG---GTCTGGAACGCTTATCGACGCAATTGGCATCTACGTCCACC 471

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RESULT      6
S45168
LOCUS      S45168      724 bp      mRNA      PLN      08-MAY-1993
DEFINITION salt=15 kda organ-specific salt-induced protein [Oryza sativa=rice,
var. Indica, cv Taichung native 1, roots, mRNA, 724 nt].
ACCESSION  S45168
VERSION    S45168.1  GI:256637

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KEYWORDS .

SOURCE Oryza sativa roots var. Indica cv Taichung native 1.

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 724)

AUTHORS Claes,B., Dekeyser,R., Villarroel,R., Van den Bulcke,M., Bauw,G.,
Van Montagu,M. and Caplan,A.

TITLE Characterization of a rice gene showing organ-specific expression
in response to salt stress and drought

JOURNAL Plant Cell 2 (1), 19-27 (1990)

MEDLINE 93005642

REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 115368] from the original journal article.
This sequence comes from Fig. 2.

FEATURES Location/Qualifiers

source 1..724
/organism="Oryza sativa"
/db_xref="taxon:4530"

gene 29..466
/gene="salt"
/note="15 kda organ-specific salt-induced protein"

CDS 29..466
/gene="salt"
/note="15 kda organ-specific salt-induced protein; Method:
conceptual translation with partial peptide sequencing;
This sequence comes from Fig. 4"
/codon_start=1
/protein_id="AAB23484.1"
/db_xref="GI:256638"
/translation="MTLVKIGLWGGNGGSAQDISVPPKLLGVTTIYSSDAIRSI AFNY
IGVDGQEYAIGPWGGEGTSTEIKLSSEHIKEISGTHGPVYDLADIVTYLKIVTSAN
NTYEAGVPNGKEFSIPLQDSGHVVGFFGRSGTLIDAIGIYVHP"

BASE COUNT 198 a 156 c 170 g 200 t

ORIGIN

Query Match 15.6%; Score 65.4; DB 8; Length 724;
Best Local Similarity 50.9%; Pred. No. 0.00056;
Matches 209; Conservative 0; Mismatches 193; Indels 9; Gaps 2;

Qy 2 gagaggggaggggtcggcgcaggacatcgcaacaacggagccgcccaggcgtctgcaaaacc 61
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Db 60 GAAATGGAGGGTCAGCTCAGGACATC-----AGTGTGCCACCCAAGAAGCTTCTAGGCG 113

Qy 62 tgaccgtccgccccggcggttgccgtggactccatcgagttcacctacaccgacacaggtg 121
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Db 114 TGACAATCTACAGCTCAGATGCAATCAGATCCATTGCCTTCAACTATATCGGTGTGGATG 173

Qy 122 gccagacgcgcaccgctgggcatgggggtggacttgccggcaacgtccggaagctcgatc 181
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Db 174 GACAGGAATATGCCATTGGTCCATGGGGTGGGGGCGAAGGCACCTCTACAGAGATTAAAT 233

Qy 182 ttggcgacgctgaatacgtcaaggaagtttctggaacgtacggcgcatctcgaaggtgcga 241
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Db 234 TGGGCTCCTCTGAGCATATTAAGGAGATTTCTGGAACCCATGGCCCAGTCTATGATCTGG 293

Qy	242	ctaccctgacctcgttgaggattgtcaccagcaccgccagagcttggggggccatggggca	301
Db	294	CTGACATTGTCACCTATCTTAAGATCGTGACAAGTGCTAATAATACATACGAGGCTGGAG	353
Qy	302	tcnagagcgggacacggtttctgcatcancggcaccatcgggcagcagcatcgtgggattct	361
Db	354	TCCCAAATGGAAAGGAATTCAGCATTCCTGCAAGACTCTGGCCATGTCGTTGGATTCT	413
Qy	362	atggacgcgcgacgaacaggctcgtcgctgcgatcgggtgtctacctgcgcc	412
Db	414	TTGGAAG---GTCTGGAACGCTTATCGACGCAATTGGCATCTACGTCCACC	461

RESULT 7

HVVU237754

LOCUS	HVU237754	623 bp	mRNA	PLN	09-APR-1999
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DEFINITION Hordeum vulgare high light-induced mRNA for putative lectin (18kDa).

ACCESSION AJ237754

VERSION AJ237754.1 GI:4584684

KEYWORDS h1#2 gene; putative lectin.

SOURCE barley.

ORGANISM *Hordeum vulgare*

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 623)

AUTHORS Potter, E., Beator, J. and Kloppstech, K.

TITLE The expression of mRNAs for light-stress proteins in barley:
inverse relationship of mRNA levels of individual genes within the
leaf gradient

JOURNAL *Planta* 199 (2), 314-320 (1996)

MEDLINE 96275958

REFERENCE 2 (bases 1 to 623)

AUTHORS Klopptech, K.R.

TITLE Direct Submission

JOURNAL Submitted (07-APR-1999) Kloppstech K.R., Institut fuer Botanik,
University of Hannover, Herrenhaeuser Str. 2, 30419 Hannover,
GERMANY

FEATURES

Location/Qualifiers

source

1. .623

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/organism="Hordeum vulgare"
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/cultivar="apex"

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/db xref="taxon:4513"
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/tissue type="Primary leaf"
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gene

35. $\overline{.517}$

/gene="hl#2"

CDS

35. .517

/gene="h1#2"

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/codon start=1
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/product="putative lectin"
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/protein id="CAB40792.1"
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/db xref="GI:4584685"
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/translation="MSSSPVVKLGPWGGDDGVAHDITVAPQRLESITIRWGKVLHSPA  
FTYRDKDNQLHTAGPWGGAGGEKEDPDTITLGPSEYITQVDWSVGPFKLKEIEHCITS  
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BASE COUNT 127 a 183 c 184 g 129 t
ORIGIN

Query Match 15.5%; Score 64.8; DB 8; Length 623;
Best Local Similarity 51.5%; Pred. No. 0.00078;
Matches 209; Conservative 0; Mismatches 179; Indels 18; Gaps 2;

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Qy      2 gagagggaggggtcgggcgaggacatcgcaacaacggagccgagggcgtctgcaaaacc 61
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Db      69 GGGGGGGGCGACGACGGGTGGCCCCACGACATCACGGTGGCGCCGCGAGCGGCTGGAGAGCA 128

Qy     62 tgaccgtccgccccggcggttgccgtggactccatcgagttcacctacaccgacacaggtg 121
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    129 TCACCATCCGCTGGGGCAAGGTCTGCACTCCGTCGCCTTCACCTACAGGGACAAGGACA 188

Qy    122 gccagacgcgcaccgctggggcgatgggggtggacttggcgg-----caacgtccgga 172
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    189 ACCAGCTGCACACCGCCGGGCCCTGGGGCGGCGCCGGAGGGGAGAAGGAAGACCCGGACA 248

Qy    173 agctcgatcttggcgacgctgaatacgtcaaggaagtttctggaacgtacggcgcatte- 231
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    249 CGATCACGTTGGGCCCCCTCGGAGTACATAACTCAGGTCGACTGGTCGGTGGGACCGTTCA 308

Qy    232 -----gaaggtgcgactaccctgacctcggttgaggattgtcaccagcaccgccagag 283
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    309 AGCTCAAGGAGATCGAGCACTGCATCACCTCGCTCAAGTTTGTGACCAACCAGGCCAGCT 368

Qy    284 cttggggggccatggggcatcnagagcgggacacgttttctgcatcancggcaccatcggca 343
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    369 ACGGCCCCGTTTCGGGTACGCGGTGGACAGCACGCACTACAGCCTGCCCGTGCTCAACAACG 428

Qy    344 gcagcatcgtgggattctatggaacgcgcgacgaacaggctcgtcgc 389
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    429 GCAGCGTCGTCGGCATGTTTCGGCCGCGCCGGAGACTACCTCCACGC 474
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RESULT 8

TAU32427

LOCUS TAU32427 1209 bp mRNA PLN 20-MAY-1996

DEFINITION Triticum aestivum clone WCI-1 unknown mRNA, complete cds.

ACCESSION U32427

VERSION U32427.1 GI:1323741

KEYWORDS .

SOURCE wheat.

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 1209)

AUTHORS Gorlach,J., Volrath,S., Knauf-Beiter,G., Hengy,G., Beckhove,U.,
Kogel,K.-H., Oostendorp,M., Staub,T., Ward,E., Kessman,H. and
Ryals,J.

TITLE Benzothiadiazole, a novel class of inducers of systemic acquired
resistance, activates gene expression and disease resistance in
wheat

JOURNAL Plant Cell 8 (4), 629-643 (1996)
 MEDLINE 96206814
 REFERENCE 2 (bases 1 to 1209)
 AUTHORS Volrath,S., Gorlach,J., Ward,E. and Ryals,J.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUL-1995) Sandra Volrath, Crop Protection, Ciba
 Agricultural Biotechnology, 3054 Cornwallis Road, Research Triangle
 Park, NC 27709, USA
 FEATURES Location/Qualifiers
 source 1. .1209
 /organism="Triticum aestivum"
 /strain="Kanzler"
 /db_xref="taxon:4565"
 /clone="WCI-1"
 CDS 27. .1058
 /codon_start=1
 /product="unknown"
 /protein_id="AAC49284.1"
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 ENWFICFNMVFDVRRFMGSSFKVMGDFRGNEGEWAIVGGTGEFAYAQGVITFNKTWSA
 QANVRELHVRALCLSFSKAPETPCSRTPRESSVTKIGPWGKISGEFLDVPTTPQRLEC
 VTIRHGVVIDSLAFSFDQAGGQHNVGPGWGGPCGDNDKDTIKLGPSEIVTEVSGTIGVF
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 polyA_site 1209
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 BASE COUNT 301 a 305 c 292 g 311 t
 ORIGIN

Query Match 14.8%; Score 61.8; DB 8; Length 1209;
 Best Local Similarity 52.9%; Pred. No. 0.0027;
 Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
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Db      659 GACACCACAACGTCTAGAGTGTGTGACCATTCGCCATGGAGTTGTCATTGATTCACTTGC 718

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      719 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 778

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      779 CGGGGACAACAAGGACACGATTAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 838

Qy     216 aacgtacggcgcatcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      839 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 898

Qy     267 caccagcaccgccagagcttgggggccatggggcatcnagagcgggacacgtttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      899 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 958

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
  
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Db    959 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1015

Qy    387 cgctgcgatcgggtgtctacctgcgccaactt 417
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Db    1016 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1046

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RESULT      9
AR016814
LOCUS       AR016814      1250 bp      DNA              PAT      05-DEC-1998
DEFINITION  Sequence 39 from patent US 5777200.
ACCESSION   AR016814
VERSION     AR016814.1   GI:3973091
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1250)
  AUTHORS   Ryals,J.A., Alexander,D.C., Goodman,R.M. and Stinson,J.R.
  TITLE     Chemically regulatable and anti-pathogenic DNA sequences and uses
            thereof
  JOURNAL    Patent: US 5777200-A 39 07-JUL-1998;
FEATURES             Location/Qualifiers
     source             1. .1250
                       /organism="unknown"
BASE COUNT      327 a      310 c      299 g      314 t
ORIGIN

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Query Match          14.8%;   Score 61.8;   DB 6;   Length 1250;
Best Local Similarity 52.9%;   Pred. No. 0.0026;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy    39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
      | | ||      |||| |      |||| | |||| | | |||| | | || | |
Db    673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy    99 gttcacctacaccgacacaggtggccagacgcgcaccgctggggcgatgggggtggacttgg 158
      || ||| | | |||| | |||| | | || |||| | |||| |||| | |
Db    733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy    159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
      ||| || | | | | | | |||| | || | | | |||| |||| |
Db    793 CGGGGACAACAAGGACACGATTAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy    216 aacgtacggcgcatcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
      |||| | | | || | || | || | | | | | | | | | | | |
Db    853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy    267 caccagcaccgccagagcttggggggccatggggcatcnagagcgggacacgttttctgcat 326
      |||| | | | | | | |||| | || | | | |||| |||| | |
Db    913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy    327 cancggcaccatcggcagcagcatcgtgggattctatggacgcgcgacgaacaggctcgt 386
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Db    973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

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Db 1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060

RESULT 11

AR027163

LOCUS AR027163 1250 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 39 from patent US 5856154.

ACCESSION AR027163

VERSION AR027163.1 GI:5938003

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1250)

AUTHORS Ryals, J.A., Alexander, D.C., Goodman, R.M. and Ward, E.R.

TITLE Method of protecting plants from oomycete pathogens

JOURNAL Patent: US 5856154-A 39 05-JAN-1999;

FEATURES Location/Qualifiers

source 1. .1250

/organism="unknown"

BASE COUNT 327 a 310 c 299 g 314 t

ORIGIN

Query Match 14.8%; Score 61.8; DB 6; Length 1250;

Best Local Similarity 52.9%; Pred. No. 0.0026;

Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy 39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy 99 gttcacctacaccgacacaggtggccagacgcgcaccgctggggcgatgggggtggacttgg 158
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy 159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttcttgg 215
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 793 CGGGGACAACAAGGACACGATTAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy 216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy 267 caccagcaccgccagagcttgggggccatggggcatcnagagcgggacacgtttcttgc 326
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy 327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacagggtcgt 386
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy 387 cgctgcgatcggtgtctacctgcgccaaactt 417
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060
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RESULT 12
 AR038450
 LOCUS AR038450 1250 bp DNA PAT 29-SEP-1999
 DEFINITION Sequence 39 from patent US 5804693.
 ACCESSION AR038450
 VERSION AR038450.1 GI:5957167
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1250)
 AUTHORS Gaffney,T.D., Ryals,J.A., Friedrich,L.B., Uknes,S.J., Ward,E.R.,
 Kessmann,H. and Vernooij,B.T.
 TITLE Chemically regulatable and anti-pathogenic DNA sequences and uses
 thereof
 JOURNAL Patent: US 5804693-A 39 08-SEP-1998;
 FEATURES Location/Qualifiers
 source 1. .1250
 /organism="unknown"
 BASE COUNT 327 a 310 c 299 g 314 t
 ORIGIN

Query Match 14.8%; Score 61.8; DB 6; Length 1250;
 Best Local Similarity 52.9%; Pred. No. 0.0026;
 Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      733 ATTTTCCTTCGTGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      793 CGGGGACAACAAGGACACGATTAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
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Db      853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy     267 caccagcaccgccagagcttggggggccatggggcactnagagcgggacacggtttctgcat 326
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Db      913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
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Db      973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy     387 cgctgcgatcggtgtctacctgcgccaactt 417
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Db     1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060
  
```

RESULT 13

AR064592
 LOCUS AR064592 1250 bp DNA PAT 29-SEP-1999
 DEFINITION Sequence 39 from patent US 5847258.
 ACCESSION AR064592
 VERSION AR064592.1 GI:5993900
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1250)
 AUTHORS Ryals,J.A., Moyer,M.B., Payne,G.B. and Ward,E.R.
 TITLE DNA encoding .beta.-1,3-glucanases
 JOURNAL Patent: US 5847258-A 39 08-DEC-1998;
 FEATURES Location/Qualifiers
 source 1. .1250
 /organism="unknown"
 BASE COUNT 327 a 310 c 299 g 314 t
 ORIGIN

Query Match 14.8%; Score 61.8; DB 6; Length 1250;
 Best Local Similarity 52.9%; Pred. No. 0.0026;
 Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

Qy 39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
 | | | | | | | | | | | | | | | | | | | | | |
 Db 673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732
 Qy 99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcatgggggtggacttgg 158
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 Db 733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792
 Qy 159 cggcaacgtccggaa---gctcgatcttgccgacgctgaatacgtcaaggaagtttctg 215
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 Db 793 CGGGGACAACAAGGACACGATTAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852
 Qy 216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
 | | | | | | | | | | | | | | | | | | | | | |
 Db 853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912
 Qy 267 caccagcaccgccagagcttggggggccatggggcatcnagagcgggacacgtttctgcat 326
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 Db 913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972
 Qy 327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
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 Qy 387 cgctgcgatcggtgtctacctgcgccaactt 417
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 Db 1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060

RESULT 14
 AR067517
 LOCUS AR067517 1250 bp DNA PAT 29-SEP-1999
 DEFINITION Sequence 39 from patent US 5851766.

ACCESSION AR067517
 VERSION AR067517.1 GI:5998739
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1250)
 AUTHORS Ryals,J.A. and Harms,C.
 TITLE Process for isolating chemically regulatable DNA sequences
 JOURNAL Patent: US 5851766-A 39 22-DEC-1998;
 FEATURES Location/Qualifiers
 source 1. .1250
 /organism="unknown"
 BASE COUNT 327 a 310 c 299 g 314 t
 ORIGIN

Query Match 14.8%; Score 61.8; DB 6; Length 1250;
 Best Local Similarity 52.9%; Pred. No. 0.0026;
 Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

Qy 39 gccgccgagggcgtctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
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 Db 673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

 Qy 99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcatgggggtggacttgg 158
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 Qy 159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
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 Db 793 CGGGGACAACAAGGACACGATTAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

 Qy 216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
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 Qy 267 caccagcaccgccagagcgttgggggcatggggcatcnagagcgggacacgttttctgcat 326
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 Qy 327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
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 Db 973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

 Qy 387 cgctgcgatcggtgtctacctgcgccaaactt 417
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060

RESULT 15
 I38469
 LOCUS I38469 1250 bp DNA PAT 13-MAY-1997
 DEFINITION Sequence 39 from patent US 5614395.
 ACCESSION I38469
 VERSION I38469.1 GI:2084523
 KEYWORDS .

SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1250)
 AUTHORS Ryals,J.A., Alexander,D.C., Beck,J.J., Duesing,J.H., Goodman,R.M.,
 Friedrich,L.B., Harms,C., Meins,F. Jr., Montoya,A. deceased,
 Moyer,M.B., Neuhaus,J., Payne,G.B., Sperisen,C., Stinson,J.R.,
 Uknes,S.J., Ward,E.R. and Williams,S.C.
 TITLE Chemically regulatable and anti-pathogenic DNA sequences and uses
 thereof
 JOURNAL Patent: US 5614395-A 39 25-MAR-1997;
 FEATURES Location/Qualifiers
 source 1. .1250
 /organism="unknown"
 BASE COUNT 327 a 310 c 299 g 314 t
 ORIGIN

Query Match 14.8%; Score 61.8; DB 6; Length 1250;
 Best Local Similarity 52.9%; Pred. No. 0.0026;
 Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggtgccgtggactccatcga 98
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcatgggggtggacttgg 158
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Db      733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctg 215
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      793 CGGGGACAACAAGGACACGATTAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcatcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy     267 caccagcaccgccagagcttggggggccatggggcatcnagagcgggacacgtttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgcgaacaggctcgt 386
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Db      973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy     387 cgctgcgatcgggtgtctacctgcgccaactt 417
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060
  
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Search completed: February 7, 2002, 11:10:50
 Job time: 10176 sec

OM nucleic - nucleic search, using sw model

Run on: February 7, 2002, 11:00:37 ; Search time 428.31 Seconds
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836.688 Million cell updates/sec

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Perfect score: 418
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

No.	Score	Match	Length	DB	ID	Description
1	61.8	14.8	1250	16	AAQ99794	Wheat gene WCI-1.
2	61.8	14.8	1250	20	AAV62847	Wheat WCI-1 gene f
3	61.8	14.8	1250	20	AAV81628	Wheat gene WCI-1.
c 4	38	9.1	1162	16	AAQ99797	Wheat gene WCI-3.
c 5	38	9.1	1162	20	AAV62849	Wheat WCI-3 gene f
c 6	38	9.1	1162	20	AAV81631	Wheat gene WCI-3 c
c 7	37.8	9.0	1907	22	AAH14960	Human cDNA sequenc
c 8	37	8.9	638	21	AAC76206	Human ORFX ORF1761
c 9	36.8	8.8	732	22	AAH07780	Human cDNA clone (
c 10	36	8.6	567	21	AAA29550	HIV codon altered
11	36	8.6	734	20	AAZ09144	H. tuberosus lecti
c 12	36	8.6	2838	18	AAT85067	Human cytomegalovi
c 13	36	8.6	2838	18	AAT85073	Human cytomegalovi
14	35.2	8.4	748	22	AAD11123	Human small cell l
15	35.2	8.4	1201	22	AAD11122	Human small cell l
16	34	8.1	268	21	AAA67597	Eucalyptus grandis
17	34	8.1	356	21	AAA67606	Eucalyptus grandis
18	34	8.1	362	21	AAA67608	Eucalyptus grandis
19	34	8.1	399	21	AAA67609	Eucalyptus grandis
20	34	8.1	462	21	AAA67607	Eucalyptus grandis
21	33.8	8.1	1875	22	AAH65378	C glutamicum codin
22	33.8	8.1	1878	22	AAH21088	C. glutamicum DNA
23	33.8	8.1	2142	22	AAF71364	Corynebacterium gl
24	33.8	8.1	4080	22	AAH21086	C. glutamicum DNA
c 25	33.8	8.1	4590	22	AAH24065	Yeast AOD9604-asso
26	33.8	8.1	349980	22	AAH68525	C glutamicum codin
c 27	33.4	8.0	1134	15	AAQ58821	NANBH virus gene f
c 28	33.4	8.0	77536	21	AAA14651	Nucleotide sequenc
29	33.2	7.9	1588	15	AAQ58010	Sequence of cellul
30	33.2	7.9	1588	21	AAA95410	Trichoderma reesei
31	33.2	7.9	1680	16	AAQ97715	Endoglucanase-I ge
32	33.2	7.9	1680	16	AAQ91283	T. longibrachiatum
33	33.2	7.9	1680	17	AAT32222	Trichoderma endogl
34	33.2	7.9	1696	6	AAN50179	Sequence of endogl
35	33	7.9	306	18	AAT85880	Malassezia fungus
36	33	7.9	400	19	AAV64545	M. tuberculosis im
37	33	7.9	400	19	AAV44436	Mycobacterium tube
38	33	7.9	400	20	AAZ19346	M. tuberculosis an
39	33	7.9	400	20	AAZ19134	M. tuberculosis re
40	33	7.9	427	18	AAT85904	Malassezia fungus
41	33	7.9	109519	22	AAS08693	Micromonospora DNA
42	32.8	7.8	645	21	AAC58874	Human tumour suppr
43	32.6	7.8	3723	21	AAZ39009	Mouse Escl coding
44	32.6	7.8	5082	21	AAZ39008	Mouse Escl full le
45	32.6	7.8	5144	21	AAZ39025	Mouse EsclL coding

ALIGNMENTS

RESULT 1
 AAQ99794
 ID AAQ99794 standard; cDNA; 1250 BP.
 XX
 AC AAQ99794;

XX
 DT 19-JUN-1996 (first entry)
 XX
 DE Wheat gene WCI-1.
 XX
 KW SAR; tobacco; protein-synthesis independent gene; cyclohexamide;
 KW systemic acquired resistance response; anti-pathogen; plant protection;
 KW wheat; WCI-1; ss.
 XX
 OS Triticum aestivum.
 XX
 PN WO9519443-A2.
 XX
 PD 20-JUL-1995.
 XX
 PF 03-JAN-1995; 95WO-IB00002.
 XX
 PR 13-JAN-1994; 94US-0181271.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Alexander DC, Ryals JA, Uknes SJ, Ward ER;
 XX
 DR WPI; 1995-263872/34.
 XX
 PT New DNA contg. plant systemic acquired resistance genes - and
 PT transgenic plants contg. them, impart disease and pest resistance,
 PT also Arabidopsis gene promoter to control DNA transcription
 XX
 PS Claim 17; Page 53-4; 85pp; English.
 XX
 CC This sequence represents the DNA sequence of a wild-type wheat gene that
 CC can be chemically induced in plants. This gene is designated WCI-1.
 CC This sequence, and AAQ99795-Q99799 are all used in recombinant/chimaeric
 CC wheat DNA molecules of the invention. These sequences were isolated by
 CC differential screening of a cDNA library, followed by analysis by
 CC Northern hybridisation to RNA in the presence and absence of
 CC cyclohexamide. The genes are used in the creation of transgenic plants.
 CC Transgenic expression of 2 or more of the recombinant molecules of the
 CC invention that encode anti-pathogenic proteins provides a synergistic
 CC increase in plant protection, and may also offer protection against a
 CC wider range of pathogens.
 XX
 SQ Sequence 1250 BP; 327 A; 310 C; 299 G; 314 T; 0 other;

Query Match 14.8%; Score 61.8; DB 16; Length 1250;
 Best Local Similarity 52.9%; Pred. No. 2.3e-07;
 Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

Qy 39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 673 gacaccacaacgtctagagtgtgtgaccattcgccatggagttgtcattgattcacttgc 732
 Qy 99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatgggggtggacttgg 158
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 Db 733 attttccttcgtcgaccaagctggtggacaacataacgttggcccatgggggtgggcatg 792

Qy	159	cggcaacgtccggaa---gctcgatccttggcgacgctgaatacgtcaaggaagtttctgg	215
Db	793	cggggacaacaaggacacgattaaacttgggtccatcgagattgtgacagaagtctctgg	852
Qy	216	aacgtacggcgcatcgaaggtgcgactaccctgacct-----cgttgaggattgt	266
Db	853	aacgattggtgtatttggagcagccaatgtcgagtacaatgccataacatcactaaccat	912
Qy	267	caccagcaccgccagagcttgggggccatggggcatcnagagcgggacacgtttctgcat	326
Db	913	taccacaaatgtccgcacgtacggggccttggagaaccgcagtgactcgtttcagtg	972
Qy	327	cancggcaccatcggcgacgacatcgtgggattctatggacgcgcgacgaacaggctcgt	386
Db	973	tcccgtgcaggacaaaagcagcatcgtgggttcttctgtgtgcgctaggaa---atacgt	1029
Qy	387	cgctgcgatcgggtgtctacctgcgccaactt	417
Db	1030	ggaggcgctcgggggtttacgtgtgtccacct	1060

RESULT 2

ID AAV62847 standard; cDNA; 1250 BP.

AC AAV62847;

DT 05-MAR-1999 (first entry)

DE Wheat WCI-1 gene fragment.

KW Chemically regulatable DNA promoter; expression control; pesticide;

XX

XX

XX

XX

XX

XX

XX

XX

XX

PT for chemically controlling expression in transformed plants

PS Example 58B; Column 223-226; 175pp; English.

CC This sequence is a fragment of the wheat WCI

CC isolated using the method of the invention. The method is for isolating a
 CC chemically regulatable DNA promoter fragment from the 5' flanking region
 CC of a chemically regulatable gene in a plant tissue. The method allows
 CC isolation of sequences which will be useful for the controlled expression
 CC of genes, under the control of a non-coding regulatable sequence. This is
 CC useful in plants with a herbicide or pesticide detoxification mechanism
 CC under the control of a chemical regulator, the regulator being applied
 CC before or with the herbicide or pesticide to give optimal tolerance. The
 CC promoter fragment is useful for controlling sequences which encode traits
 CC such as height, shape, development, male or female sterility, and the
 CC ability of the plant to withstand cold, heat, salt and drought. The
 CC chemical induction of the promoter allows the regulation of production of
 CC compounds, e.g. flavours, fragrances, pigments, natural sweeteners,
 CC industrial feedstocks, antimicrobials and pharmaceuticals, by
 CC biosynthesis or metabolite conversion, whose biosynthesis is controlled
 CC by endogenous or foreign genes. The method allows control over the time
 CC and rate of gene expression either throughout the whole plant, or in
 CC localized tissues, to achieve e.g. fungal or insect resistance by for
 CC instance dusting the leaves with the chemical regulator. Controlling the
 CC developmental processes by the application of a regulating chemical in
 CC e.g. the commercial production of cultivated crops allows processes such
 CC as germination, flower formation and fruit ripening to be synchronised at
 CC a given time.

XX

SQ Sequence 1250 BP; 327 A; 310 C; 299 G; 314 T; 0 other;

Query Match 14.8%; Score 61.8; DB 20; Length 1250;
 Best Local Similarity 52.9%; Pred. No. 2.3e-07;
 Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

Qy 39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
 | | | | | | | | | | | | | | | | | | | | | |
 Db 673 gacaccacaacgtctagagtgtgtgaccattcgccatggagttgtcattgattcacttgc 732

Qy 99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcatgggggtggacttgg 158
 | | | | | | | | | | | | | | | | | | | | | |
 Db 733 attttccttcgtcgaccaagctggtggacaacataacgttggcccatgggggtgggcatg 792

Qy 159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctg 215
 | | | | | | | | | | | | | | | | | | | | | |
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Qy 216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
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Qy 267 caccagcaccgccagagcttgggggcatggggcatcnagagcgggacacgtttctgcat 326
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 Db 913 taccacaaatgtccgcacgtacgggccctttggagaaccgcagtggtactcgtttcagtg 972

Qy 327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
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 Db 973 tcccgtgcaggacaaaagcagcatcggtgggtttcttcgtgtgcgctaggaa---atacgt 1029

Qy 387 cgctgcgatcggtgtctacctgcgccaactt 417
 | | | | | | | | | | | | | | | | | | | | | |

Db 1030 ggaggcgctcgggggtttacgtgtgtccacct 1060

RESULT 3

AAV81628

ID AAV81628 standard; cDNA; 1250 BP.

XX

AC AAV81628;

XX

DT 25-FEB-1999 (first entry)

XX

DE Wheat gene WCI-1.

XX

KW Regulation; transcription; plant tissue; chimeric construction; PR;

KW pathogenesis-related protein; anti-pathogenic; transgenic plant;

KW beta-1,3-glucanase activity; pest resistance; ss.

XX

OS Triticum sp.

XX

PN US5847258-A.

XX

PD 08-DEC-1998.

XX

PF 31-MAY-1995; 95US-0457364.

XX

PR 31-MAY-1995; 95US-0457364.

PR 08-MAR-1988; 88US-0165667.

PR 06-FEB-1989; 89US-0305566.

PR 24-MAR-1989; 89US-0329018.

PR 20-JUN-1989; 89US-0368672.

PR 20-OCT-1989; 89US-0425504.

PR 07-SEP-1990; 90US-0580431.

PR 21-DEC-1990; 90US-0632441.

PR 01-APR-1991; 91US-0678378.

PR 27-SEP-1991; 91US-0768122.

PR 06-MAR-1992; 92US-0848506.

PR 06-NOV-1992; 92US-0973197.

PR 06-APR-1993; 93US-0042847.

PR 12-APR-1993; 93US-0045957.

PR 16-JUL-1993; 93US-0093301.

PR 13-JAN-1994; 94US-0181271.

XX

PA (NOVS) NOVARTIS FINANCE CORP.

XX

PI Moyer MB, Payne GB, Ryals JA, Ward ER;

XX

DR WPI; 1999-059180/05.

XX

PT DNA encoding pathogenesis-related glucanase proteins - useful for
PT producing transgenic plants with enhanced disease or pest resistance

XX

PS Example 58; Column 217-220; 169pp; English.

XX

CC The present invention describes a DNA molecule encoding a
CC pathogenesis-related (PR) protein having beta-1,3-glucanase activity
CC selected from PR-2, PR-2', PR-2'', PR-N, PR-O and PR-O'. Also described
CC are: (i) a chimeric gene comprising the above DNA molecule linked to a

CC heterologous promoter; (ii) a vector containing the chimeric gene;
CC (iii) a host cell containing the chimeric gene; (iv) a transgenic plant
CC containing the chimeric gene; and (v) a seed from the transgenic plant.
CC The DNA molecule is used to produce transgenic plants with enhanced
CC disease or pest resistance. The present sequence represents a wheat
CC WCI-1 gene from the present invention.

XX

SQ Sequence 1250 BP; 327 A; 310 C; 299 G; 314 T; 0 other;

Query Match 14.8%; Score 61.8; DB 20; Length 1250;
Best Local Similarity 52.9%; Pred. No. 2.3e-07;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

```
Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggtgccgtggactccatcga 98
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     673 gacaccacaacgtctagagtgtgtgaccattcgccatggagttgtcattgattcacttgc 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcatgggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     733 attttccttcgtcgaccaagctggtggacaacataacgttggcccatgggggtgggcatg 792

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctg 215
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     793 cggggacaacaaggacacgattaaacttggtccatcggagattgtgacagaagtctctg 852

Qy     216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     853 aacgattggtgtatttggagcagccaatgtcgagtacaatgccataacatcactaaccat 912

Qy     267 caccagcaccgccagagcttgggggcatggggcatcnagagcgggacacgtttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     913 taccacaaatgtccgcacgtacgggccctttggagaaccgcagtgtactcgtttcagtg 972

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     973 tcccgtgcaggacaaaagcagcatcggtgggtttcttcgtgtgcgctaggaa---atacgt 1029

Qy     387 cgctgcgatcgggtgtctacctgcgccaaactt 417
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1030 ggaggcgctcgggggtttacgtgtgtccacct 1060
```

RESULT 4

AAQ99797/c

ID AAQ99797 standard; cDNA; 1162 BP.

XX

AC AAQ99797;

XX

DT 19-JUN-1996 (first entry)

XX

DE Wheat gene WCI-3.

XX

KW SAR; tobacco; protein-synthesis independent gene; cyclohexamide;

KW systemic acquired resistance response; anti-pathogen; plant protection;

KW wheat; WCI-3; ss.

XX

OS Triticum aestivum.
 XX
 PN WO9519443-A2.
 XX
 PD 20-JUL-1995.
 XX
 PF 03-JAN-1995; 95WO-IB00002.
 XX
 PR 13-JAN-1994; 94US-0181271.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Alexander DC, Ryals JA, Uknes SJ, Ward ER;
 XX
 DR WPI; 1995-263872/34.
 XX
 PT New DNA contg. plant systemic acquired resistance genes - and
 PT transgenic plants contg. them, impart disease and pest resistance,
 PT also Arabidopsis gene promoter to control DNA transcription
 XX
 PS Claim 17; Page 55-56; 85pp; English.
 XX
 CC This sequence represents the DNA sequence of a wild-type wheat gene that
 CC can be chemically induced in plants. This gene is designated WCI-3.
 CC This sequence, AAQ99794-Q99796, AAQ99798 and AAQ99799 are all used in
 CC recombinant/chimaeric wheat DNA molecules of the invention. These
 CC sequences were isolated by differential screening of a cDNA library,
 CC followed by analysis by Northern hybridisation to RNA in the presence
 CC and absence of cyclohexamide. The genes are used in the creation of
 CC transgenic plants. Transgenic expression of 2 or more of the
 CC recombinant molecules of the invention that encode anti-pathogenic
 CC proteins provides a synergistic increase in plant protection, and may
 CC also offer protection against a wider range of pathogens.
 XX
 SQ Sequence 1162 BP; 313 A; 275 C; 269 G; 305 T; 0 other;

Query Match 9.1%; Score 38; DB 16; Length 1162;
 Best Local Similarity 51.9%; Pred. No. 0.51;
 Matches 140; Conservative 0; Mismatches 117; Indels 13; Gaps 2;

```

Qy   157  ggcggaacgtccggaagctcgatcttggcgacgctgaatacgtcaaggaagtttctgga 216
      || | ||||      | | | | ||||      | |      | | | |||| |||||
Db   443  GGGGACAACAAGGACACGATTAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGGA 384

Qy   217  acgtacggcgcatcgaaggtgcgactaccctg-----acctcgttgaggattgtc 267
      |||  || | ||| || | || | | | | | | | | | | | | | | | | |
Db   383  ACGATTGGTGTATTTGGAGCAGCCAATGTGCGAGTACAATGCCATAACATCACTAACCATT 324

Qy   268  accagcaccgccagagcttggggggccatggggcatcnagagcgggacacgtttctgcatc 327
      |||| | | | | | | | |||| | | | | | | | | | | | | | |
Db   323  ACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGTT 264

Qy   328  ancggcaccatcggcagcagcatcgtgggattctatggacgcgcgacgaacagggtcgtc 387
      ||      | | ||||| ||||| |||| | | |||| | ||| | |||
Db   263  CCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAATA----CGTG 208

```

Qy 388 gctgcgatcggtgtctacctgcgccaactt 417
 | | | | | | | | | | | | | | |
 Db 207 GAGGCGCTCGGGGTTTACGTGTGTCCACCT 178

RESULT 5

AAV62849/c

ID AAV62849 standard; cDNA; 1162 BP.

XX

AC AAV62849;

XX

DT 05-MAR-1999 (first entry)

XX

DE Wheat WCI-3 gene fragment.

XX

KW Chemically regulatable DNA promoter; expression control; pesticide;

KW herbicide tolerance; WCI-3 gene; wheat; ss.

XX

OS Triticum sp.

XX

PN US5851766-A.

XX

PD 22-DEC-1998.

XX

PF 31-MAY-1995; 95US-0456262.

XX

PR 31-MAY-1995; 95US-0456262.

XX

PA (NOVS) NOVARTIS FINANCE CORP.

XX

PI Harms C, Ryals JA;

XX

DR WPI; 1999-080396/07.

XX

PT Isolating chemically regulatable DNA sequences in plants - useful

PT for chemically controlling expression in transformed plants

XX

PS Example 58B; Column 227-228; 175pp; English.

XX

CC This sequence is a fragment of the wheat WCI-3 gene. This gene can be
 CC isolated using the method of the invention. The method is for isolating a
 CC chemically regulatable DNA promoter fragment from the 5' flanking region
 CC of a chemically regulatable gene in a plant tissue. The method allows
 CC isolation of sequences which will be useful for the controlled expression
 CC of genes, under the control of a non-coding regulatable sequence. This is
 CC useful in plants with a herbicide or pesticide detoxification mechanism
 CC under the control of a chemical regulator, the regulator being applied
 CC before or with the herbicide or pesticide to give optimal tolerance. The
 CC promoter fragment is useful for controlling sequences which encode traits
 CC such as height, shape, development, male or female sterility, and the
 CC ability of the plant to withstand cold, heat, salt and drought. The
 CC chemical induction of the promoter allows the regulation of production of
 CC compounds, e.g. flavours, fragrances, pigments, natural sweeteners,
 CC industrial feedstocks, antimicrobials and pharmaceuticals, by
 CC biosynthesis or metabolite conversion, whose biosynthesis is controlled
 CC by endogenous or foreign genes. The method allows control over the time
 CC and rate of gene expression either throughout the whole plant, or in

CC localized tissues, to achieve e.g. fungal or insect resistance by for
CC instance dusting the leaves with the chemical regulator. Controlling the
CC developmental processes by the application of a regulating chemical in
CC e.g. the commercial production of cultivated crops allows processes such
CC as germination, flower formation and fruit ripening to be synchronised at
CC a given time.

XX

SQ Sequence 1162 BP; 313 A; 275 C; 269 G; 305 T; 0 other;

Query Match 9.1%; Score 38; DB 20; Length 1162;
Best Local Similarity 51.9%; Pred. No. 0.51;
Matches 140; Conservative 0; Mismatches 117; Indels 13; Gaps 2;

```
Qy 157 ggcggcaacgtccggaagctcgatcttggcgacgctgaatacgtcaaggaagtttctgga 216
    || || || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 443 GGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGGA 384

Qy 217 acgtacggcgcatcgaaggtgcgactaccctg-----acctcgttgaggattgtc 267
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 383 ACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCATT 324

Qy 268 accagcaccgccagagcttggggggccatggggcgcacnagagcgggacacgtttctgcatc 327
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 323 ACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGTT 264

Qy 328 ancggcaccatcggcagcagcatcgtgggattctatggacgcgcgacgaacaggctcgtc 387
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 263 CCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAATA----CGTG 208

Qy 388 gctgcgatcgggtgtctacctgcgccaactt 417
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 207 GAGGCGCTCGGGGTTTACGTGTGTCCACCT 178
```

RESULT 6

AAV81631/c

ID AAV81631 standard; cDNA; 1162 BP.

XX

AC AAV81631;

XX

DT 25-FEB-1999 (first entry)

XX

DE Wheat gene WCI-3 cDNA sequence.

XX

KW Regulation; transcription; plant tissue; chimeric construction; PR;

KW pathogenesis-related protein; anti-pathogenic; transgenic plant;

KW beta-1,3-glucanase activity; pest resistance; ss.

XX

OS Triticum sp.

XX

PN US5847258-A.

XX

PD 08-DEC-1998.

XX

PF 31-MAY-1995; 95US-0457364.

XX

PR	31-MAY-1995;	95US-0457364.
PR	08-MAR-1988;	88US-0165667.
PR	06-FEB-1989;	89US-0305566
PR	24-MAR-1989;	89US-0329018.
PR	20-JUN-1989;	89US-0368672.
PR	20-OCT-1989;	89US-0425504.
PR	07-SEP-1990;	90US-0580431.
PR	21-DEC-1990;	90US-0632441.
PR	01-APR-1991;	91US-0678378.
PR	27-SEP-1991;	91US-0768122.
PR	06-MAR-1992;	92US-0848506.
PR	06-NOV-1992;	92US-0973197.
PR	06-APR-1993;	93US-0042847.
PR	12-APR-1993;	93US-0045957.
PR	16-JUL-1993;	93US-0093301.
PR	13-JAN-1994;	94US-0181271.

PA (NOVS) NOVARTIS FINANCE CORP.

PI Moyer MB, Payne GB, Ryals JA, Ward ER;

DR WPI; 1999-059180/05.

PT DNA encoding pathogenesis-related glucanase proteins - useful for
PT producing transgenic plants with enhanced disease or pest resistance

PS Example 58; Column 221-222; 169pp; English.

CC The present invention describes a DNA molecule encoding a
CC pathogenesis-related (PR) protein having beta-1,3-glucanase activity
CC selected from PR-2, PR-2', PR-2'', PR-N, PR-O and PR-O'. Also described
CC are: (i) a chimeric gene comprising the above DNA molecule linked to a
CC heterologous promoter; (ii) a vector containing the chimeric gene;
CC (iii) a host cell containing the chimeric gene; (iv) a transgenic plant
CC containing the chimeric gene; and (v) a seed from the transgenic plant.
CC The DNA molecule is used to produce transgenic plants with enhanced
CC disease or pest resistance. The present sequence represents the wheat
CC gene WCI-3 cDNA sequence from the present invention.

SQ Sequence 1162 BP; 313 A; 275 C; 269 G; 305 T; 0 other;

Query Match 9.1%; Score 38; DB 20; Length 1162;
Best Local Similarity 51.9%; Pred. No. 0.51;
Matches 140; Conservative 0; Mismatches 117; Indels 13; Gaps 2;

Qy	157	ggcggaacgtccggaagctcgatcttggcgacgctgaatacgtcaaggaagtttctgga	216
Db	443	GGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGGA	384
Qy	217	acgtacggcgcatctcgaaggtgcgactaccctg-----acctcgttgaggattgtc	267
Db	383	ACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCATT	324
Qy	268	accagcaccgccagagcttgggggccatggggcatcnagagcgggacacgtttctgcac	327
Db	323	ACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGTT	264

Qy 328 ancggcaccatcggcagcagcatcgtgggattctatggacgcgcgacgaacaggctcgtc 387
 || | ||||| |||| | |||| | ||| | |||
 Db 263 CCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAATA----CGTG 208

Qy 388 gctgcgatcgggtgtctacctgcgccaactt 417
 | ||| |||| | ||| | | | | |
 Db 207 GAGGCGCTCGGGGTTTACGTGTGTCCACCT 178

RESULT 7

AAH14960/c

ID AAH14960 standard; cDNA; 1907 BP.

XX

AC AAH14960;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human cDNA sequence SEQ ID NO:12876.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-0116126.

XX

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -

XX

PS Claim 8; SEQ ID 12876; 2537pp + CD ROM; English.

XX

CC The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX

SQ Sequence 1907 BP; 273 A; 685 C; 625 G; 324 T; 0 other;

Query Match 9.0%; Score 37.8; DB 22; Length 1907;
Best Local Similarity 49.2%; Pred. No. 0.64;
Matches 96; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Qy 204 ggaagtttctggaacgtacggcgcatcgaaggtgcgactaccctgacctcggtgaggat 263
||| | | ||| | | | | | | | | | | | | | |
Db 545 GGAGGCTGCTGGCCCCAGAGCTCCTCCAGCAGGGCCACGCCTCCTCCCCGCTCTGCGG 486

Qy 264 tgtcaccagcaccgccagagcttgggggcatggggcatcnagagcgggacacgtttctg 323
| | | | | | | | | | | | | | | | | | | |
Db 485 CTGCCGGCTGCACACCCAGGCCTGCGTGTGCGGCGGCAGCGCGCTCAGGAAGTGTTCAG 426

Qy 324 catcancggcaccatcggcagcagcatcggtggattctatggacgcgcgacgaacaggct 383
|| | | | | | | | | | | | | | | | | | | |
Db 425 CACCAGCAGCTCCAACATCTGCTCCTTGGTGTGCACCTCGGGCCGCGGCCAGTCCCGGCA 366

Qy 384 cgtcgctgcatcg 398
| | | | |
Db 365 CAGGGCGCGGAGCAG 351

RESULT 8

AAC76206/c

ID AAC76206 standard; cDNA; 638 BP.

XX

AC AAC76206;

XX

DT 08-FEB-2001 (first entry)

XX

DE Human ORFX ORF1761 polynucleotide sequence SEQ ID NO:3521.

XX

KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiatic;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;

KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI; 2000-602362/57.
 DR P-PSDB; AAB41997.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PS Claim 5; Page 2686-2687; 5507pp; English.
 XX
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianaemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 SQ Sequence 638 BP; 120 A; 232 C; 181 G; 104 T; 1 other;

Query Match 8.9%; Score 37; DB 21; Length 638;
Best Local Similarity 51.2%; Pred. No. 0.83;
Matches 85; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

```
Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      494 GCGGTTGAAGGGTCTGGCANTCCTCCTCGGCCTCCCTGGGGTTCTCCAGGTCTGTGCCGC 435

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      434 GAGGGTTGCCCTCGGCCCGCCGGTCCATGCCACCTCCAGGAGGCCAGCAGGTGCTTGG 375

Qy     159 cggcaacgtccggaagctcgatcttggcgacgctgaatacgtcaag 204
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     374 CAGAGCCGTCCAGGGGTAGGATCTTGGAGGAGATGAAGTCCTCTAG 329
```

RESULT 9

AAH07780/c

ID AAH07780 standard; cDNA; 732 BP.

XX

AC AAH07780;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human cDNA clone (5'-primer) SEQ ID NO:4615.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-0116126.

XX

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -

XX

PS Claim 1; SEQ ID 4615; 2537pp + CD ROM; English.

XX

CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX

SQ Sequence 732 BP; 123 A; 232 C; 277 G; 94 T; 6 other;

Query Match 8.8%; Score 36.8; DB 22; Length 732;

Best Local Similarity 48.7%; Pred. No. 0.96;

Matches 95; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 204 ggaagtttctggaacgtacggcgcatcgaaggtgcgactaccctgacctcggttgaggat 263

Db 545 GGAGGCTGCTGGCCCCAGAGCTCCTCCAGCAGGGCCACCGCCTCCTCCCCGCTCTGCGG 486

Qy 264 tgtcaccagcaccgccagagcttgggggccatggggcatcnagagcgggacacgtttctg 323

Db 485 CTGCCGGCTGCACACCCAGGCCTGCGTGTGCGCGGGCAGCGCGCTCAGGAAGTGTTCAG 426

Qy 324 catcancggcaccatcggcagcagcatcgtgggattctatggacgcgcgacgaacaggct 383

Db 425 CACCAGCAGCTCCAACATNTGCTCCTTGGTGTGCACCTCGGGCCGCGGCCAGTCCCGGCA 366

Qy 384 cgtcgctgcgatcgg 398

Db 365 CAGGGCGCGGAGCAG 351

RESULT 10

AAA29550/c

ID AAA29550 standard; DNA; 567 BP.

XX

AC AAA29550;

XX

DT 09-AUG-2000 (first entry)

XX

DE HIV codon altered env nucleotide sequence #2.
 XX
 KW Erythropoietin; EPO; G-CSF; granulocyte colony stimulating factor;
 KW wobble; codon altered gene; shuffling; modification; vaccine;
 KW insulin; peptide hormone; growth factor; cytokine; interferon;
 KW interleukin; leukaemia inhibitory factor; oncostatin M;
 KW transcription activator; expression activator; infectious organism; ds.
 XX
 OS Human immunodeficiency virus type 1.
 OS Synthetic.
 XX
 PN WO200018906-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 28-SEP-1999; 99WO-US22588.
 XX
 PR 29-SEP-1998; 98US-0102362.
 PR 29-JAN-1999; 99US-0117729.
 PR 05-FEB-1999; 99US-0118813.
 PR 24-JUN-1999; 99US-0141049.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Patten PA, Liu L, Stemmer WPC;
 XX
 DR WPI; 2000-303449/26.
 XX
 PT Novel methods for recombining codon-altered libraries of nucleic acids
 PT used to produce new proteins and new vectors with reduced rates of
 PT reversion to wild type -
 XX
 PS Example; Fig 18A; 92pp; English.
 XX
 CC A method has been developed of making codon altered nucleic acids (NAs),
 CC comprising providing a NA sequence (NA1) which encodes a polypeptide
 CC (P1), providing codon altered NA sequences, each encoding P1 or a
 CC modified form of it, and recombining the codon altered NA sequences to
 CC produce a target codon altered NA which encodes a second protein.
 CC The method of the invention can be used for recombining codon-altered
 CC libraries of nucleic acids to produce new proteins, which have
 CC improvements in a desirable characteristic. Target nucleic acids
 CC include those coding for therapeutic proteins such as erythropoietin
 CC (EPO), insulin, peptide hormones, growth factors, cytokines, interferons,
 CC interleukins, leukaemia inhibitory factor, and oncostatin M, as well as
 CC transcription and expression activators and proteins from infectious
 CC organisms for use as vaccines. The method can also be used to produce
 CC attenuated viruses which have reduced rates of reversion to wild type.
 CC The present sequence represents an HIV codon altered env nucleotide
 CC sequence, which is used in an example from the present invention.
 XX
 SQ Sequence 567 BP; 32 A; 129 C; 222 G; 184 T; 0 other;

Query Match 8.6%; Score 36; DB 21; Length 567;
 Best Local Similarity 48.5%; Pred. No. 1.5;
 Matches 96; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

CC quantities. This sequence encodes the plant, H. tuberosus, lectin
CC descibed in the method of the invention.
XX
SQ Sequence 734 BP; 227 A; 124 C; 165 G; 218 T; 0 other;

Query Match 8.6%; Score 36; DB 20; Length 734;
Best Local Similarity 51.3%; Pred. No. 1.6;
Matches 134; Conservative 0; Mismatches 121; Indels 6; Gaps 2;

```
Qy      62 tgaccgtccgccccggcggttgccgtggactccatcgagttcacctacaccgacacaggtg 121
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     110 taaacgtccgtagtggagctattgttgatgccatctactttggctacacgga---aggtg 166

Qy     122 gccagacgcgcaccgctgggcgatggggtggacttggcggcaacgtccggaagctcgatc 181
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     167 gtatcagctacgagactgccatttttgggtggtcgtaatggcagcctttctacgattgaca 226

Qy     182 ttggcgacgtgaatacgtcaaggaagtttctggaacgtacggcgcatctgaaggtgcga 241
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     227 ttgccgacgatgaggagatcatcgagattaacggaaaagtgggaactcttga---gaacc 283

Qy     242 ctaccctgacctcggttgaggattgtcaccagcaccgccagagcttggggggccatggggca 301
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     284 taaaccttgtctcgcaattgactttcgtgaccaacaacaaacctatggaccatattggca 343

Qy     302 tcnagagcgggacacgtttct 322
      | | | | | | | | | |
Db     344 cgaatggagggacagatttct 364
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RESULT 12
AAT85067/c
ID AAT85067 standard; DNA; 2838 BP.
XX
AC AAT85067;
XX
DT 18-MAR-1998 (first entry)
XX
DE Human cytomegalovirus (HCMV) UL70 open reading frame.
XX
KW Human cytomegalovirus primase; HCMV; screening; inhibitor; infection;
KW diagnosis; antiviral; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2838
FT /*tag= a
FT /note= "stop codon not shown in specification"
XX
PN GB2311068-A.
XX
PD 17-SEP-1997.
XX
PF 05-MAR-1997; 97GB-0004575.
XX

PR 04-APR-1996; 96GB-0007118.
 PR 14-MAR-1996; 96US-0013389.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Gotlib L, Hazuda DJ, Lafemina RL;
 XX
 DR WPI; 1997-427906/40.
 DR P-PSDB; AAW27083.
 XX
 PT Novel human cytomegalovirus helicase - used for screening for HCMV
 PT antivirals and in diagnosis of HCMV related diseases
 XX
 PS Claim 2; Pages 11-12; 28pp; English.
 XX
 CC The present sequence represents DNA encoding human cytomegalovirus
 CC (HCMV) UL70, spanning nucleotides 103373 through 100536 of HCMV
 CC AD169 which was amplified by PCR primers AAT85065-6. The amplified
 CC product was digested with NdeI and XmaI and cloned into NdeI/XmaI
 CC digested pB8T7H6 vector DNA to yield the plasmid pB8T7H6 UL70. The
 CC amplified HCMV UL70 orf sequence and its translational product were
 CC determined. Recombination into BacPAK 6 viral DNA, plaque purification
 CC and generation of viral stocks were by standard protocols. The protein
 CC product was used with a new HCMV helicase in a screening assay for
 CC compounds which inhibit HCMV helicase (preferably with an IC50 of not
 CC greater than 200nM), and as a diagnostic tool for diseases resulting
 CC from HCMV infection.
 XX
 SQ Sequence 2838 BP; 511 A; 1057 C; 748 G; 522 T; 0 other;

Query Match 8.6%; Score 36; DB 18; Length 2838;
 Best Local Similarity 50.6%; Pred. No. 2.1;
 Matches 87; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

```

Qy      22 gacatcgcaacaacggagccgcccaggcgtctgcaaaacctgaccgtccgccccggcggtt 81
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      846 GTCAGCGTCGTAAGCCACCACGCGCCGGTACTCGAGCAACCGCGCGGTGCCAGCGCCGT 787

Qy      82 gccgtggactccatcgagttcacctacaccgacacaggtggccagacgcgcaccgctggg 141
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      786 GCGGTAGGCCAGGTAGACGTAGTGCACGCAGACAGTGTCTGGGCAGACGCGCACGTTTCGCG 727

Qy     142 cgatgggggtggacttggcggcaacgtccggaagctcgatcttggcgacgctg 193
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      726 GAACGCGTTGATCTGCGTGTCCACCTGCTCTAGCTCGGTGTAGTCGCGGCGG 675

```

RESULT 13
 AAT85073/c
 ID AAT85073 standard; DNA; 2838 BP.
 XX
 AC AAT85073;
 XX
 DT 18-MAR-1998 (first entry)
 XX
 DE Human cytomegalovirus (HCMV) primase DNA.

XX
 KW Human cytomegalovirus primase; HCMV; screening; inhibitor; infection;
 KW diagnosis; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2838
 FT /*tag= a
 FT /product= Human_cytomegalovirus_primase
 FT /note= "stop codon not shown in specification"
 XX
 PN GB2311069-A.
 XX
 PD 17-SEP-1997.
 XX
 PF 05-MAR-1997; 97GB-0004577.
 XX
 PR 04-APR-1996; 96GB-0007117.
 PR 14-MAR-1996; 96US-0013546.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Gotlib L, Hazuda DJ, Lafemina RL;
 XX
 DR WPI; 1997-427907/40.
 DR P-PSDB; AAW27085.
 XX
 PT Novel human cytomegalovirus primase - used for screening for HCMV
 PT antivirals and in diagnosis of HCMV related diseases
 XX
 PS Claim 2; Pages 11-12; 28pp; English.
 XX
 CC The present sequence represents DNA encoding a new human cytomegalovirus
 CC (HCMV) primase. A screening assay for compounds which inhibit HCMV
 CC primase (preferably with an IC50 of not greater than 200nM), comprises
 CC incubation of the compound with the primase. The primase of the invention
 CC is useful as a screening tool for HCMV antivirals, and as a diagnostic
 CC tool for diseases resulting from HCMV infection.
 XX
 SQ Sequence 2838 BP; 511 A; 1057 C; 748 G; 522 T; 0 other;

Query Match 8.6%; Score 36; DB 18; Length 2838;
 Best Local Similarity 50.6%; Pred. No. 2.1;
 Matches 87; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 22 gacatcgcaacaacggagccgcccggcgtctgcaaaacctgaccgtccgccccggcggtt 81
 | | | | | | | | | | | | | | | | | | | | | |
 Db 846 GTCAGCGTCGTAAGCCACCACGCGCCGGTACTCGAGCAACGCGCGCGTGCCAGCGCCGT 787
 Qy 82 gccgtggactccatcgagttcacctacaccgacacaggtggccagacgcgcaccgctggg 141
 | | | | | | | | | | | | | | | | | | | | | |
 Db 786 GCGGTAGGCCAGGTAGACGTAGTGCACGCAGACAGTGTGCGGCAGACGCGCACGTTTCGCG 727
 Qy 142 cgatgggggtggacttggcgggcaacgtccggaagctcgatcttggcgacgctg 193
 | | | | | | | | | | | | | | | | | | | | | |

Db 726 GAACGCGTTGATCTGCGTGTCCACCTGCTCTAGCTCGGTGTAGTCGCGGCGG 675

RESULT 14

AAD11123

ID AAD11123 standard; DNA; 748 BP.

XX

AC AAD11123;

XX

DT 24-SEP-2001 (first entry)

XX

DE Human small cell lung cancer associated gene, DKFZp434C196 #2.

XX

KW Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA;
KW melanoma; cancer; colon; breast; head; neck; transitional cancer;
KW leiomyosarcoma; synovial sarcoma; cytostatic; ds.

XX

OS Homo sapiens.

XX

PN WO200153349-A2.

XX

PD 26-JUL-2001.

XX

PF 19-JAN-2001; 2001WO-US02015.

XX

PR 21-JAN-2000; 2000US-0489101.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PA (CORR) CORNELL RES FOUND INC.

XX

PI Stockert E, Scanlan MJ, Jager D, Old LJ, Gure AO, Chen Y;

XX

DR WPI; 2001-457597/49.

XX

PT Isolated polypeptide, used to treat or prognose a disorder
PT characterized by expression of a hCAAP e.g. cancer, is encoded by an
PT isolated nucleic acid comprising an NA Group 3 or 4 molecule -

XX

PS Claim 57; Page 116; 152pp; English.

XX

CC The invention relates to nucleic acids and encoded polypeptides which
CC are cancer associated antigens expressed in patients afflicted with
CC small cell lung cancer. The molecules provided by the invention can be
CC used in the diagnosis, monitoring, research or treatment of conditions
CC characterised by the expression of one or more cancer associated
CC antigens. The polypeptide is used to treat a disorder characterised by
CC expression of a hCAAP, and determine regression, progression or onset
CC of a condition characterised by expression of an abnormal amount of a
CC protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders
CC are small and non-small cell lung cancer, melanoma, colon, breast, head
CC and neck, or transitional cancer, leiomyosarcoma or synovial sarcoma.
CC The present sequence is human DKFZp434C196 DNA. This small cell lung
CC cancer associated gene is designated as NY-SCLC-13.

XX

SQ Sequence 748 BP; 166 A; 261 C; 246 G; 72 T; 3 other;

Query Match 8.4%; Score 35.2; DB 22; Length 748;
 Best Local Similarity 54.7%; Pred. No. 2.6;
 Matches 70; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

```

Qy      14 cggcgcaggacatcgcaacaacggagccgagcgctctgcaaaacctgaccgtccgcc 73
          | | | | | | | | | | | | | | | | | | | | | |
Db      52 ccgaccagggcatcgctaattgaggacaccacccagtgcatcgccaacgaggaagccgccc 111

Qy      74 cggcgcttgccgtggactccatcgagttcacctacaccgacacaggtggccagacgcgca 133
          | | | | | | | | | | | | | | | | | | | | | |
Db     112 agggcatcgccgaggagcgcctccagggcatcgccaacgaggaggttgcccagggcatcg 171

Qy     134 ccgctggg 141
          | | | | |
Db     172 ccaatggg 179
  
```

RESULT 15

AAD11122

ID AAD11122 standard; DNA; 1201 BP.

XX

AC AAD11122;

XX

DT 24-SEP-2001 (first entry)

XX

DE Human small cell lung cancer associated gene, DKFZp434C196 #1.

XX

KW Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA;

KW melanoma; cancer; colon; breast; head; neck; transitional cancer;

KW leiomyosarcoma; synovial sarcoma; cytostatic; ds.

XX

OS Homo sapiens.

XX

PN WO200153349-A2.

XX

PD 26-JUL-2001.

XX

PF 19-JAN-2001; 2001WO-US02015.

XX

PR 21-JAN-2000; 2000US-0489101.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PA (CORR) CORNELL RES FOUND INC.

XX

PI Stockert E, Scanlan MJ, Jager D, Old LJ, Gure AO, Chen Y;

XX

DR WPI; 2001-457597/49.

XX

PT Isolated polypeptide, used to treat or prognose a disorder

PT characterized by expression of a hCAAP e.g. cancer, is encoded by an

PT isolated nucleic acid comprising an NA Group 3 or 4 molecule -

XX

PS Claim 57; Page 114-115; 152pp; English.

XX

CC The invention relates to nucleic acids and encoded polypeptides which

CC are cancer associated antigens expressed in patients afflicted with
 CC small cell lung cancer. The molecules provided by the invention can be
 CC used in the diagnosis, monitoring, research or treatment of conditions
 CC characterised by the expression of one or more cancer associated
 CC antigens. The polypeptide is used to treat a disorder characterised by
 CC expression of a hCAAP, and determine regression, progression or onset
 CC of a condition characterised by expression of an abnormal amount of a
 CC protein encoded by a nucleic acid (NA) Group 1 molecule. The disorders
 CC are small and non-small cell lung cancer, melanoma, colon, breast, head
 CC and neck, or transitional cancer, leiomyosarcoma or synovial sarcoma.
 CC The present sequence is human DKFZp434C196 DNA. This small cell lung
 CC cancer associated gene is designated as NY-SCLC-13.

XX

SQ Sequence 1201 BP; 255 A; 377 C; 349 G; 178 T; 42 other;

Query Match 8.4%; Score 35.2; DB 22; Length 1201;
 Best Local Similarity 54.7%; Pred. No. 2.9;
 Matches 70; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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Qy 74 ccggcggttgccgtggactccatcgagttcacctacaccgacacaggtggccagacgcgca 133
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Db 112 agggcatcgccgaggacgccatccagggcatcgccaacgaggaggttgcccagggcatcg 171

Qy 134 ccgctggg 141
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Db 172 ccaatggg 179
  
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	61.8	14.8	1250	1	US-08-181-271A-39	Sequence 39, Appl
	2	61.8	14.8	1250	1	US-08-449-315-39	Sequence 39, Appl
	3	61.8	14.8	1250	1	US-08-444-803-39	Sequence 39, Appl
	4	61.8	14.8	1250	1	US-08-449-043-39	Sequence 39, Appl
	5	61.8	14.8	1250	1	US-08-456-265A-39	Sequence 39, Appl
	6	61.8	14.8	1250	1	US-08-455-416-39	Sequence 39, Appl
	7	61.8	14.8	1250	1	US-08-455-244-39	Sequence 39, Appl
	8	61.8	14.8	1250	1	US-08-454-876-39	Sequence 39, Appl
	9	61.8	14.8	1250	2	US-08-457-364-39	Sequence 39, Appl
	10	61.8	14.8	1250	2	US-08-456-262-39	Sequence 39, Appl
	11	61.8	14.8	1250	2	US-08-456-240-39	Sequence 39, Appl
	12	61.8	14.8	1250	2	US-08-455-736-39	Sequence 39, Appl
	13	61.8	14.8	1250	2	US-08-971-217-39	Sequence 39, Appl
	14	61.8	14.8	1250	4	US-09-350-600-39	Sequence 39, Appl
c	15	38	9.1	1162	1	US-08-181-271A-42	Sequence 42, Appl
c	16	38	9.1	1162	1	US-08-449-315-42	Sequence 42, Appl
c	17	38	9.1	1162	1	US-08-444-803-42	Sequence 42, Appl
c	18	38	9.1	1162	1	US-08-449-043-42	Sequence 42, Appl
c	19	38	9.1	1162	1	US-08-456-265A-42	Sequence 42, Appl
c	20	38	9.1	1162	1	US-08-455-416-42	Sequence 42, Appl
c	21	38	9.1	1162	1	US-08-455-244-42	Sequence 42, Appl
c	22	38	9.1	1162	1	US-08-454-876-42	Sequence 42, Appl
c	23	38	9.1	1162	2	US-08-457-364-42	Sequence 42, Appl
c	24	38	9.1	1162	2	US-08-456-262-42	Sequence 42, Appl
c	25	38	9.1	1162	2	US-08-456-240-42	Sequence 42, Appl
c	26	38	9.1	1162	2	US-08-455-736-42	Sequence 42, Appl
c	27	38	9.1	1162	2	US-08-971-217-42	Sequence 42, Appl
c	28	38	9.1	1162	4	US-09-350-600-42	Sequence 42, Appl
	29	34.4	8.2	396	4	US-09-060-756-325	Sequence 325, App
c	30	33.6	8.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	31	33.2	7.9	1201	2	US-08-169-948B-13	Sequence 13, Appl
	32	33.2	7.9	1201	2	US-08-448-873-13	Sequence 13, Appl

33	33.2	7.9	1201	4	US-08-382-452D-13	Sequence 13, Appl
34	33.2	7.9	1527	1	US-08-380-438-1	Sequence 1, Appli
35	33.2	7.9	1588	2	US-08-389-564B-16	Sequence 16, Appl
36	33.2	7.9	1588	3	US-08-466-047B-16	Sequence 16, Appl
c 37	33.2	7.9	4411529	4	US-09-103-840A-1	Sequence 1, Appli
c 38	32.4	7.8	666	6	5472691-4	Patent No. 5472691
c 39	32.4	7.8	669	3	US-08-556-965-1	Sequence 1, Appli
c 40	32.4	7.8	723	6	5472691-7	Patent No. 5472691
c 41	32.4	7.8	1389	2	US-08-023-980B-3	Sequence 3, Appli
c 42	32.4	7.8	1389	2	US-08-486-953A-3	Sequence 3, Appli
c 43	32.4	7.8	1396	6	5472691-1	Patent No. 5472691
c 44	32.4	7.8	10079	2	US-08-476-866-20	Sequence 20, Appl
c 45	32.4	7.8	43280	2	US-08-804-227C-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-181-271A-39
; Sequence 39, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/181,271A

; FILING DATE: 13-JAN-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
US-08-181-271A-39

Query Match 14.8%; Score 61.8; DB 1; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcatgggggtggacttgg 158
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Db      733 ATTTTCCTTCGTTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctg 215
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Db      793 CGGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcattcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
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Db      853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy     267 caccagcaccgccagagcttggggggccatggggcatcnagagcgggacacgttttctgcat 326
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Db      913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
      | | | | | | | | | | | | | | | | | | | | | |
Db      973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy     387 cgctgcgatcggtgtctacctgcgccaaactt 417
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Db     1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060
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RESULT 2
US-08-449-315-39
; Sequence 39, Application US/08449315
; Patent No. 5650505
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,315
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-449-315-39

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Query Match          14.8%; Score 61.8; DB 1; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
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Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy     159 cggcaacgtccggaa---gctcgatcttgccgacgctgaatacgtcaaggaagtttctgg 215
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      793 CGGGGACAACAAGGACACGATTAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy     267 caccagcaccgccagagcttgggggccatggggcatcnagagcgggacacgtttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacagggtcgt 386
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy     387 cgctgcgatcggtgtctacctgcgccaaactt 417
      | | | | | | | | | | | | | | | | | | | | | | | |
Db     1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060

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RESULT 3
US-08-444-803-39
; Sequence 39, Application US/08444803
; Patent No. 5654414
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,803
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-444-803-39

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Query Match          14.8%; Score 61.8; DB 1; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatgggggtggacttgg 158
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Db      733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

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Qy 159 cggcaacgtccggaa---gctcgatcttggcgacgtgaatacgtcaaggaagtttctgg 215
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 Db 793 CGGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy 216 aacgtacggcgcatcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
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 Db 853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy 267 caccagcaccgccagagcttgggggcatggggcatcnagagcgggacacgtttctgcat 326
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 Db 913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy 327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
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 Db 973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy 387 cgctgcgatcggtgtctacctgcgccaaactt 417
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 Db 1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060

RESULT 4

US-08-449-043-39

; Sequence 39, Application US/08449043

; Patent No. 5689044

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,043
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-449-043-39

Query Match 14.8%; Score 61.8; DB 1; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

```
Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatgggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     793 CGGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy     267 caccagcaccgccagagcttggggggccatggggcactnagagcgggacacgtttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy     387 cgctgcgatcggtgtctacctgcgccaaactt 417
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060
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RESULT 5
US-08-456-265A-39
; Sequence 39, Application US/08456265A
; Patent No. 5767369
; GENERAL INFORMATION:
; APPLICANT: Alexander, Danny C.
; APPLICANT: Ryals, John A.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Stinson, Jeffrey R.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation

;
; STREET: 520 White Plains Road, P.O. Box 2005
;
; CITY: Tarrytown
;
; STATE: New York
;
; COUNTRY: USA
;
; ZIP: 10591
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,265A
;
; FILING DATE: 31-MAY-95
;
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/181,271
;
; FILING DATE: 13-JAN-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
;
; FILING DATE: 16-JUL-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
;
; FILING DATE: 6-NOV-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
;
; FILING DATE: 1-APR-1991
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
;
; FILING DATE: 6-FEB-1989
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
;
; FILING DATE: 8-MAR-1988
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
;
; FILING DATE: 6-APR-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
;
; FILING DATE: 21-DEC-1990
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
;
; FILING DATE: 20-OCT 1989
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
;
; FILING DATE: 6-MAR-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
;
; FILING DATE: 27-SEP-1991
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
;
; FILING DATE: 7-SEP-1990
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
;
; FILING DATE: 20-JUN-1989
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
;
; FILING DATE: 24-MAR-1989
;
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-456-265A-39

```

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Query Match          14.8%; Score 61.8; DB 1; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
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Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcatgggggtggacttgg 158
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Db      733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctg 215
      | | | | | | | | | | | | | | | | | | | | | |
Db      793 CGGGGACAACAAGGACACGATTAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcatcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
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Db      853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy     267 caccagcaccgccagagcttggggggccatggggcatcnagagcgggacacgttttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | |
Db      913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgcacgaacaggctcgt 386
      | | | | | | | | | | | | | | | | | | | | | |
Db      973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy     387 cgctgcgatcggtgtctacctgcgccaactt 417
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Db     1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060

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RESULT 6
US-08-455-416-39
; Sequence 39, Application US/08455416
; Patent No. 5777200
; GENERAL INFORMATION:

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; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,416
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-455-416-39

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Query Match          14.8%; Score 61.8; DB 1; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
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Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatgggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      793 CGGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcatcgaaggtgcgactaccctgacct-----cgttgaggattgt 266

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Db	853	AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT	912
Qy	267	caccagcaccgccagagccttgggggccatggggcactnagagcgggacacgtttctgcat	326
Db	913	TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT	972
Qy	327	cancggcaccatcggcagcagcatcgtgggattctatggacgcgcgacgaacaggctcgt	386
Db	973	TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTCCTCGTGTGCGCTAGGAA---ATACGT	1029
Qy	387	cgctgcgatcgggtgtctacctgcgccaactt	417
Db	1030	GGAGGCGCTCGGGGTTTACGTGTGTCCACCT	1060

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RESULT 7
US-08-455-244-39
; Sequence 39, Application US/08455244
; Patent No. 5789214
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,244
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
US-08-455-244-39

Query Match 14.8%; Score 61.8; DB 1; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
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Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcatgggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | |
Db      733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
      | | | | | | | | | | | | | | | | | | | | | |
Db      793 CGGGGACAACAAGGACACGATTAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcatcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
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Db      853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy     267 caccagcaccgccagagcttggggggccatggggcatcnagagcgggacacgtttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | |
Db      913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
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Db      973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy     387 cgctgcgatcggtgtctacctgcgccaaactt 417
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Db     1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060
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RESULT 8

US-08-454-876-39

; Sequence 39, Application US/08454876

; Patent No. 5804693

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,876
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:


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; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-454-876-39

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Query Match          14.8%; Score 61.8; DB 1; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcatgggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      793 CGGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy     267 caccagcaccgccagagcttgggggccatggggcatcnagagcgggacacgttttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacagggtcgt 386
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy     387 cgctgcgatcggtgtctacctgcgccaactt 417
      | | | | | | | | | | | | | | | | | | | | | | | |
Db     1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060

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RESULT 9

US-08-457-364-39

; Sequence 39, Application US/08457364

; Patent No. 5847258

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/457,364

; FILING DATE: 31-MAY-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/181,271

; FILING DATE: 13-JAN-94

; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,197

; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/678,378

; FILING DATE: 1-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/305,566

; FILING DATE: 6-FEB-1989

; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-457-364-39

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Query Match          14.8%; Score 61.8; DB 2; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
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Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctggggcgatgggggtggacttgg 158
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Db      733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

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Qy 159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
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Db 793 CGGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy 216 aacgtacggcgcatcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
    ||| | | | | | | | | | | | | | | | | | | | | |
Db 853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy 267 caccagcaccgccagagcttggggggccatggggcatcnagagcgggacacgtttctgcat 326
    ||| | | | | | | | | | | | | | | | | | | | | |
Db 913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy 327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
    || | | | | | | | | | | | | | | | | | | | | |
Db 973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy 387 cgctgcatcggtgtctacctgcgccaactt 417
    | ||| ||| || ||| || | | | | | |
Db 1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060

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RESULT 10

US-08-456-262-39

; Sequence 39, Application US/08456262

; Patent No. 5851766

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,262
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689

```
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1250 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-08-456-262-39
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Query Match          14.8%; Score 61.8; DB 2; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;
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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
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Db     673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatgggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | | | |
Db     733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
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Db     793 CGGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
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Db     853 AACGATTGGTGTATTTGGAGCAGCCAATGTGAGTACAATGCCATAACATCACTAACCAT 912

Qy     267 caccagcaccgccagagcttgggggcatggggcatcnagagcgggacacgtttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | | | |
Db     913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
      | | | | | | | | | | | | | | | | | | | | | | | |
Db     973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy     387 cgctgcatcggtgtctacctgcgccaactt 417
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Db    1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060
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RESULT 11
US-08-456-240-39
; Sequence 39, Application US/08456240
; Patent No. 5856154
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
```

; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,240
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-456-240-39

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Query Match          14.8%; Score 61.8; DB 2; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
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Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      793 CGGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy     267 caccagcaccgccagagcttgggggcatggggcactnagagcgggacacgttttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
      | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA--ATACGT 1029

Qy 387 cgctgcatcggtgtctacctgcgccaactt 417
 | ||| |||| || ||| || | || |

Db 1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060

RESULT 12

US-08-455-736-39

; Sequence 39, Application US/08455736

; Patent No. 5880328

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/455,736

; FILING DATE: 31-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/181,271

; FILING DATE: 13-JAN-1994

; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,197

; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-455-736-39

```

```

Query Match          14.8%; Score 61.8; DB 2; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy      39 gccgccgaggcgtctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98

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Db    673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy    99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | |
Db    733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy    159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
      | | | | | | | | | | | | | | | | | | | | | |
Db    793 CGGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy    216 aacgtacggcgcatcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
      | | | | | | | | | | | | | | | | | | | | | |
Db    853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy    267 caccagcaccgccagagcttgggggccatggggcatcnagagcgggacacgtttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | |
Db    913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy    327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
      | | | | | | | | | | | | | | | | | | | | | |
Db    973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy    387 cgctgcgatcggtgtctacctgcgccaactt 417
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Db    1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060

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RESULT 13

US-08-971-217-39

; Sequence 39, Application US/08971217

; Patent No. 5942662

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Harms, Christian

; APPLICANT: Friedrich, Leslie

; APPLICANT: Beck, James

; APPLICANT: Uknes, Scott

; APPLICANT: Ward, Eric

; TITLE OF INVENTION: INDUCIBLE HERBICIDE RESISTANCE

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5942662artis Corporation

; STREET: 3054 Cornwallis Road, P.O. Box 12257

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/971,217

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,364
; FILING DATE: 31-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/181,271
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV5/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:

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;      LENGTH: 1250 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: DNA (genomic)
US-08-971-217-39
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Query Match          14.8%;  Score 61.8;  DB 2;  Length 1250;
Best Local Similarity 52.9%;  Pred. No. 1.5e-08;
Matches 207;  Conservative 0;  Mismatches 169;  Indels 15;  Gaps 3;
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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
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Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

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Db      793 CGGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
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Db      853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy     267 caccagcaccgccagagcttgggggccatggggcatcnagagcgggacacgtttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

Qy     327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgacgaacaggctcgt 386
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Db      973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy     387 cgctgcgatcggtgtctacctgcgccaaactt 417
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Db     1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060
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RESULT 14
US-09-350-600-39
; Sequence 39, Application US/09350600
; Patent No. 6262342
; GENERAL INFORMATION:
; APPLICANT: Meins, Frederick
; APPLICANT: Shinshi, Hideaki
; APPLICANT: Wenzler, Herman
; APPLICANT: Hofsteenge, Jan
; APPLICANT: Ryals, John
; APPLICANT: Sperisen, Christoph
; TITLE OF INVENTION: DNA SEQUENCES ENCODING POLYPEPTIDES
; TITLE OF INVENTION: HAVING BETA-1,3-GLUCANASE ACTIVITY
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6262342artis Corporation
```

; STREET: 3054 Cornwallis Road, P.O. Box 12257
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,600
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/971,217
; FILING DATE: 14-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,364
; FILING DATE: 31-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/181,271
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672

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; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/381,443
; FILING DATE: 18-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/353,312
; FILING DATE: 17-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/226,303
; FILING DATE: 29-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-198250
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-350-600-39

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Query Match          14.8%; Score 61.8; DB 4; Length 1250;
Best Local Similarity 52.9%; Pred. No. 1.5e-08;
Matches 207; Conservative 0; Mismatches 169; Indels 15; Gaps 3;

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Qy      39 gccgccgaggcgctctgcaaaacctgaccgtccgccccggcggttgccgtggactccatcga 98
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Db      673 GACACCACAACGTCTAGAGTGTGTGACCATTGCCATGGAGTTGTCATTGATTCACTTGC 732

Qy      99 gttcacctacaccgacacaggtggccagacgcgcaccgctgggcgatgggggtggacttgg 158
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      733 ATTTTCCTTCGTCGACCAAGCTGGTGGACAACATAACGTTGGCCCATGGGGTGGGCCATG 792

Qy     159 cggcaacgtccggaa---gctcgatcttggcgacgctgaatacgtcaaggaagtttctgg 215
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      793 CGGGGACAACAAGGACACGATTAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGG 852

Qy     216 aacgtacggcgcatctcgaaggtgcgactaccctgacct-----cgttgaggattgt 266
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      853 AACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCAT 912

Qy     267 caccagcaccgccagagcttggggggccatggggccatcnagagcgggacacgttttctgcat 326
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      913 TACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGT 972

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Qy 327 cancggcaccatcggcagcagcatcggtgggattctatggacgcgcgcgaacaggctcgt 386
 || | ||||| |||| | |||| | ||| |||
 Db 973 TCCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAA---ATACGT 1029

Qy 387 cgctgcgatcggtgtctacctgcgccaactt 417
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 Db 1030 GGAGGCGCTCGGGGTTTACGTGTGTCCACCT 1060

RESULT 15

US-08-181-271A-42/c

; Sequence 42, Application US/08181271A

; Patent No. 5614395

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/181,271A

; FILING DATE: 13-JAN-94

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,197

; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:


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; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-181-271A-42

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Query Match          9.1%; Score 38; DB 1; Length 1162;
Best Local Similarity 51.9%; Pred. No. 0.073;
Matches 140; Conservative 0; Mismatches 117; Indels 13; Gaps 2;

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Qy 157 ggcggaacgtccggaagctcgatcttggcgacgctgaatacgtcaaggaagtttctgga 216

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Db    443 GGGGACAACAAGGACACGATTAAACTTGGTCCATCGGAGATTGTGACAGAAGTCTCTGGA 384

Qy    217 acgtacggcgccattcgaaggtgcgactaccctg-----acctcgttgaggattgtc 267
      ||| || | ||| | || | || | | | | | | | | | | | | | | | | | | |
Db    383 ACGATTGGTGTATTTGGAGCAGCCAATGTCGAGTACAATGCCATAACATCACTAACCATT 324

Qy    268 accagcaccgccagagcttggggggccatggggcatcnagagcgggacacgtttctgcatc 327
      |||| | | | | | | | |||| | | | | | | | | | | | | | | | | |
Db    323 ACCACAAATGTCCGCACGTACGGGCCCTTTGGAGAACCGCAGTGTACTCGTTTCAGTGTT 264

Qy    328 ancggcaccatcggcagcagcatcgtgggattctatggacgcgcgacgaacaggctcgtc 387
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Db    263 CCCGTGCAGGACAAAAGCAGCATCGTGGGTTTCTTCGTGTGCGCTAGGAATA----CGTG 208

Qy    388 gctgcgatcgggtgtctacctgcgccaactt 417
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Db    207 GAGGCGCTCGGGGTTTACGTGTGTCCACCT 178

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Search completed: February 7, 2002, 11:22:27
Job time: 7913 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2002, 08:20:58 ; Search time 4942.22 Seconds
(without alignments)
908.850 Million cell updates/sec

Title: US-09-394-745-6886
Perfect score: 418
Sequence: 1 agagaggggaggggtcggcgca.....tgtctacctgcgccaacttt 418

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
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5: em_estpl:*
 6: em_estba:*
 7: em_estro:*
 8: em_estov:*
 9: em_htc:*
 10: gb_est1:*
 11: gb_est2:*
 12: gb_htc:*
 13: gb_gss:*
 14: em_gss_fun:*
 15: em_gss_hum:*
 16: em_gss_inv:*
 17: em_gss_pln:*
 18: em_gss_pro:*
 19: em_gss_rod:*
 20: em_gss_vrt:*
 21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				Description
	No.	Score	Match	Length	DB	ID			
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c	2	402.2	96.2	632	10	AI711614			AI711614 605058C04
c	3	402.2	96.2	637	10	AI668540			AI668540 605033G04
c	4	393.2	94.1	533	10	AI670298			AI670298 605021F08
c	5	392.2	93.8	556	10	AI737987			AI737987 606044D10
c	6	291.8	69.8	582	10	AW066778			AW066778 683008F03
c	7	291.8	69.8	590	10	AW076470			AW076470 683018G06
c	8	274	65.6	587	10	AW067268			AW067268 683021C02
c	9	270.4	64.7	525	10	AW181191			AW181191 687021F05
c	10	269.4	64.4	548	10	BE225277			BE225277 946026D05
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c	12	269.4	64.4	577	10	BE510995			BE510995 946057A08
c	13	269.4	64.4	579	10	AW498242			AW498242 660044H01
	14	269.4	64.4	599	10	AW519882			AW519882 660054G12
c	15	269	64.4	577	10	AW352698			AW352698 660034E10
	16	265.4	63.5	634	10	AW566299			AW566299 660069B12
c	17	265.4	63.5	660	10	AI444678			AI444678 486015B01
	18	264.6	63.3	469	10	AW433474			AW433474 707070F07
	19	257.4	61.6	509	10	BE575013			BE575013 946090C01
c	20	256.2	61.3	515	10	AW191748			AW191748 687030C01
c	21	246.6	59.0	403	10	AI737701			AI737701 605040A10
c	22	246	58.9	553	10	AI622246			AI622246 486038E12
c	23	246	58.9	706	10	AI467693			AI467693 486015B01
c	24	245.2	58.7	494	10	BE025391			BE025391 945026C02
c	25	241.6	57.8	467	11	BG268011			BG268011 1000145E0
c	26	238	56.9	619	10	AI674034			AI674034 605041H09
c	27	235.8	56.4	562	10	AW066858			AW066858 683010F01
c	28	232.6	55.6	377	10	AI901909			AI901909 618012B10
	29	227.6	54.4	438	10	BE129595			BE129595 945026C02
c	30	226.8	54.3	416	11	BG267028			BG267028 1000110D0

c	31	223.2	53.4	452	10	AW499455	AW499455	660054G12
c	32	221	52.9	569	10	AI649927	AI649927	486099C06
c	33	216.6	51.8	381	10	AW076468	AW076468	683018G04
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c	35	200	47.8	412	10	AW202438	AW202438	687030C01
c	36	192	45.9	510	10	AW067051	AW067051	683014F07
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	38	185.6	44.4	403	10	BE512021	BE512021	946065B08
	39	185	44.3	494	10	AI881607	AI881607	606068H12
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c	41	176	42.1	424	10	BE345663	BE345663	946025A06
	42	172.4	41.2	420	10	AW179383	AW179383	618048B01
c	43	170.8	40.9	568	10	AW562891	AW562891	660069B12
c	44	168.8	40.4	571	10	AI834492	AI834492	606068H12
c	45	167.6	40.1	548	10	AW562896	AW562896	660069C11

ALIGNMENTS

RESULT 1
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 LOCUS AI657458 561 bp mRNA EST 02-FEB-2000
 DEFINITION 605003E01.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
 cDNA, mRNA sequence.
 ACCESSION AI657458
 VERSION AI657458.1 GI:4753548
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 561)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 605003 row: E column: 01.
 FEATURES Location/Qualifiers
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 /organism="Zea mays"
 /cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_lib="605 - Endosperm cDNA library from Schmidt lab"
 /tissue_type="nucellar, embryo, and endosperm"
 /dev_stage="10-14 days post-pollination"
 /lab_host="DH5(alpha)"
 /note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI;
 Site_2: XhoI; Kernel endosperm cDNA library from Schmidt"

lab"
BASE COUNT 116 a 177 c 153 g 115 t
ORIGIN

Query Match 96.2%; Score 402.2; DB 10; Length 561;
Best Local Similarity 97.6%; Pred. No. 2.5e-86;
Matches 407; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Db    469 TGACCGTCCGCGCCGGCGTTGCCGTGGACTCCATCGAGTTCACCTACACCGACACAGGTG 410

Qy    122 gccagacgcgcaccgctgggcgatgggggtggacttggcggcaacgtccggaagctcgatc 181
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Db    409 GCCAGACGCGCACCGCTGGGCGATGGGGTGGACTTGGCGGCAACGTCCGGAAGCTCGATC 350

Qy    182 ttggcgacgctgaatacgtcaaggaagtttctggaacgtacggcgcatctgaaggtgcga 241
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Db    349 TTGGCGACGCTGAATACGTCAAGGAAGTTTCTGGAACGTACGGCGCATTCGAAGGTGCGA 290

Qy    242 ctaccctgacctcggttgaggattgtcaccagcaccgccagagcttggggggccatggggca 301
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Db    289 CTACCCTGACCTCGTTGAGGATTGTCACCAGCACCGCCAGAGCTTGGGGGCCATGGGGCA 230

Qy    302 tcnagagcgggacacgtttctgcatacggcaccatcggcagcagcatcgtgggattct 361
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Db    229 TCGAGAGCGGGACACGTTTCTGCATCACCGCACCCATCGGCAGCAGCATCGTGGGATTCT 170

Qy    362 atggacgcgcgacgaacaggctcgctcgctgcgatcgggtgtctacctgcgccaacttt 418
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Db    169 ATGGACGCGCGACGACCAGGCTCGTCGCTGCGATCGGTGTCTACCTGCGCCAACCTTT 113
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RESULT 2
AI711614/c
LOCUS AI711614 632 bp mRNA EST 02-FEB-2000
DEFINITION 605058C04.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
cDNA, mRNA sequence.
ACCESSION AI711614
VERSION AI711614.1 GI:5005552
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 632)
AUTHORS Walbot, V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V

Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 605058 row: C column: 04.

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FEATURES             Location/Qualifiers
    source             1. .632
                        /organism="Zea mays"
                        /cultivar="Ohio43"
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                        /clone_lib="605 - Endosperm cDNA library from Schmidt lab"
                        /tissue_type="nucellar, embryo, and endosperm"
                        /dev_stage="10-14 days post-pollination"
                        /lab_host="DH5(alpha)"
                        /note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI;
                        Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
                        lab"
BASE COUNT           138 a      189 c      169 g      136 t
ORIGIN

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Query Match 96.2%; Score 402.2; DB 10; Length 632;
Best Local Similarity 97.6%; Pred. No. 2.6e-86;
Matches 407; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy      62 tgaccgtccgccccggcggttgccgtggactccatcgagttcacctacaccgacacaggtg 121
      |||
Db      515 TGACCGTCCGCGCCGGCGTTGCCGTGGACTCCATCGAGTTCACCTACACCGACACAGGTG 456

Qy      122 gccagacgcgcaccgctgggcgatgggggtggacttggcggcaacgtccggaagctcgatc 181
      |||
Db      455 GCCAGACGCGCACCGCTGGGCGATGGGGTGGACTTGGCGGCAACGTCCGGAAGCTCGATC 396

Qy      182 ttggcgacgctgaatacgtcaaggaagtttctggaacgtacggcgcattcgaaggtgcga 241
      |||
Db      395 TTGGCGACGCTGAATACGTCAAGGAAGTTTCTGGAACGTACGGCGCATTCTGAAGGTGCGA 336

Qy      242 ctaccctgacctcgttgaggattgtcaccagcaccgccagagcttggggggccatggggca 301
      |||
Db      335 CTACCCTGACCTCGTTGAGGATTGTCACCAGCACCGCCAGAGCTTGGGGGCCATGGGGCA 276

Qy      302 tcnagagcgggacacgttttctgcatcancggcaccatcggcagcagcatcgtgggattct 361
      |||
Db      275 TCGAGAGCGGGACACGTTTCTGCATACCGCACCCATCGGCAGCAGCATCGTGGGATTCT 216

Qy      362 atggacgcgcgacgaacaggctcgctcgctgcatcggtgtctacctgcgccaacttt 418
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Db      215 ATGGACGCGCGACGACCAGGCTCGTCGCTGCGATCGGTGTCTACCTGCGCCAACCTTT 159

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RESULT 3

AI668540/c
 LOCUS AI668540 637 bp mRNA EST 02-FEB-2000
 DEFINITION 605033G04.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
 cDNA, mRNA sequence.
 ACCESSION AI668540
 VERSION AI668540.2 GI:6031639
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 637)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 JOURNAL Unpublished (1999)
 COMMENT On May 14, 1999 this sequence version replaced gi:4827848.
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 605033 row: G column: 04.
 FEATURES Location/Qualifiers
 source 1. .637
 /organism="Zea mays"
 /cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_lib="605 - Endosperm cDNA library from Schmidt lab"
 /tissue_type="nucellar, embryo, and endosperm"
 /dev_stage="10-14 days post-pollination"
 /lab_host="DH5(alpha)"
 /note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI;
 Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
 lab"
 BASE COUNT 135 a 199 c 166 g 136 t 1 others
 ORIGIN

Query Match 96.2%; Score 402.2; DB 10; Length 637;
 Best Local Similarity 97.6%; Pred. No. 2.6e-86;
 Matches 407; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 gagagggaggggtcggcgcaggacatcgcaacaacggagccgcccagggcgtctgcaaaacc 61
 |||||
 Db 561 GAGAGGGAGGGTCGGCGCAGGACATCGCGACGACGGAGCCGCCGAGGCGTCTGCAGAACC 502
 Qy 62 tgaccgtccgccccggcggttgccgtggactccatcgagttcacctacaccgacacaggtg 121
 |||||
 Db 501 TGACCGTCCGCGCCGGCGTTGCCGTGGACTCCATCGAGTTCACCTACACCGACACAGGTG 442
 Qy 122 gccagacgcgcaccgctggggcgatgggggtggacttggcgggcaacgtccggaagctcgatc 181
 |||||
 Db 441 GCCAGACGCGCACCGCTGGGCGATGGGGTGGACTTGGCGGCAACGTCCGGAAGCTCGATC 382

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Qy 182 ttggcgacgctgaatacgtcaaggaagtttctggaacgtacggcgcatcgaaggtgcga 241
    |||
Db 381 TTGGCGACGCTGAATACGTCAAGGAAGTTTCTGGAACGTACGGCGCATTCTGAAGGTGCGA 322

Qy 242 ctaccctgacctcggttgaggattgtcaccagcaccgccagagcttgggggccatggggca 301
    |||
Db 321 CTACCCTGACCTCGTTGAGGATTGTCACCAGCACCGCCAGAGCTTGGGGGCCATGGGGCA 262

Qy 302 tcnagagcgggacacgtttctgcatcancggcaccatcggcagcagcatcgtgggattct 361
    || |||
Db 261 TCGAGAGCGGGACACGTTTCTGCATCACCGCACCCATCGGCAGCAGCATCGTGGGATTCT 202

Qy 362 atggacgcgcgacgaacaggctcgtcgctgcgatcgggtgtctacctgcgccaacttt 418
    |||
Db 201 ATGGACGCGCGACGACCAGGCTCGTCGCTGCGATCGGTGTCTACCTGCGCCAACCTTT 145

```

```

RESULT 4
AI670298/c
LOCUS AI670298 533 bp mRNA EST 02-FEB-2000
DEFINITION 605021F08.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
cDNA, mRNA sequence.
ACCESSION AI670298
VERSION AI670298.1 GI:4835072
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 533)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 605021 row: F column: 08.
FEATURES Location/Qualifiers
source 1. .533
/organism="Zea mays"
/cultivar="Ohio43"
/db_xref="taxon:4577"
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
/note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI;
Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
lab"
BASE COUNT 113 a 159 c 150 g 111 t

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ORIGIN

Query Match 94.1%; Score 393.2; DB 10; Length 533;
 Best Local Similarity 97.5%; Pred. No. 3.5e-84;
 Matches 398; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy      11 ggtcggcgaggacatcgcaacaacggagccgcccaggcgctctgcaaaacctgaccgtcc 70
          |||
Db      533 GGTCTGGCGCAGGACATCGCGACGACGGAGCCGCCGAGGCGTCTGCAGAACCTGACCGTCC 474

Qy      71 gccccggcggttgccgtggactccatcgagttcacctacaccgacacaggtggccagacgc 130
          |||
Db      473 GCGCCGGCGGTTGCCGTGGACTCCATCGAGTTCACCTACACCGACACAGGTGGCCAGACGC 414

Qy     131 gcaccgctgggagatgggggtggacttggcggcaacgtccggaagctcgatcttggcgacg 190
          |||
Db      413 GCACCGCTGGGCGATGGGGTGGACTTGGCGGCAACGTCCGGAAGCTCGATCTTGGCGACG 354

Qy     191 ctgaatacgtcaaggaagtttctggaacgtacggcgattcgaaggtgagactaccctga 250
          |||
Db      353 CTGAATACGTCAAGGAAGTTTCTGGAACGTACGGCGCATTCGAAGGTGCGACTACCCTGA 294

Qy     251 cctcggttgaggattgtcaccagcaccgccagagcttggggggccatggggcatcnagagcg 310
          |||
Db      293 CCTCGTTGAGGATTGTCACCAGCACCGCCAGAGCTTGGGGGCCATGGGGCATCGAGAGCG 234

Qy     311 ggacacgtttctgcatcaneggcaccatcggcagcagcatcggtgggattctatggacgcg 370
          |||
Db      233 GGACACGTTTCTGCATCACCGCACCCATCGGCAGCAGCATCGTGGGATTCTATGGACGCG 174

Qy     371 cgacgaacaggctcgctcgctgcatcggtgtctacctgcgccaacttt 418
          |||
Db      173 CGACGACCAGGCTCGTCGCTGCGATCGGTGTCTACCTGCGCCAACCTT 126
  
```

RESULT 5

AI737987/c

LOCUS AI737987 556 bp mRNA EST 02-FEB-2000
 DEFINITION 606044D10.x1 606 - Ear tissue cDNA library from Schmidt lab Zea
 mays cDNA, mRNA sequence.

ACCESSION AI737987

VERSION AI737987.1 GI:5070022

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 556)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University


```

LOCUS          AW066778          582 bp      mRNA          EST          12-OCT-1999
DEFINITION     683008F03.x1 683 - 14 day immature embryo from Hake lab (HS) Zea
               mays cDNA, mRNA sequence.
ACCESSION      AW066778
VERSION        AW066778.1  GI:6021850
KEYWORDS       EST.
SOURCE         Zea mays.
               ORGANISM      Zea mays
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
               clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 582)
AUTHORS        Walbot,V.
TITLE          Maize ESTs from various cDNA libraries sequenced at Stanford
               University
JOURNAL        Unpublished (1999)
COMMENT        Contact: Walbot V
               Department of Biological Sciences
               Stanford University
               855 California Ave, Palo Alto, CA 94304, USA
               Tel: 650 723 2227
               Fax: 650 725 8221
               Email: walbot@stanford.edu
               Plate: 683008 row: F column: 03.
FEATURES             Location/Qualifiers
     source           1. .582
                     /organism="Zea mays"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone_lib="683 - 14 day immature embryo from Hake lab (HS
                     )"
                     /tissue_type="embryo"
                     /dev_stage="14 days after pollination"
                     /lab_host="DH10B"
                     /note="Organ: embryo; Vector: pBKCMV (Stratagene's Zap
                     Express); Site_1: XhoI; Site_2: EcoRI; Directionally
                     cloned, 14 day immature embryo library created with
                     Stratagene's Zap Express cDNA protocol."
BASE COUNT        121 a      170 c      155 g      136 t
ORIGIN

```

Qy 182 ttggcgacgctgaatacgtcaaggaagtttctggaacgtacggcgcatcgaaggtgcga 241
 ||||| || | ||| || | || ||||| ||| ||| || |
 Db 390 TTGGCGACGCCGAGGATGTCAGGGAGGTCTCAGGAACGTACGGCACATTTGAAGGAGCCA 331

Qy 242 ctaccctgacctcggttgaggattgtcaccagcaccgccagagcttgggggcatggggca 301
 | | ||||| || ||| ||||| || | ||||| |||||
 Db 330 CCACGCTGACCTCGTTCAGAATTCTCACCAGCA---GCAGGACATGGGGGCCATGGGGCG 274

Qy 302 tcnagagcgggacacgtttctgcatcancggcaccatcggcagcagcatcgtgggattct 361
 || ||| ||||| ||||| || | ||||| ||||| |||||
 Db 273 TCGAGAACGGGACGCGTTTCTGCATCACC GCGCCGGTCGGCAGCAGCATCGTGGGGTTCT 214

Qy 362 atggacgcgcgacgaacaggctcgtcgctgcgatcgggtgtctacctgcgccaacttt 418
 ||||| ||||| | ||||| ||||| | ||||| ||||| |||||
 Db 213 ATGGACGCGCGACCAGCAGGCTCGTCGCTGCGCTTGGTGTTTACCTGCGCCGACTTT 157

RESULT 7

AW076470/c

LOCUS AW076470 590 bp mRNA EST 14-OCT-1999

DEFINITION 683018G06.xl 683 - 14 day immature embryo from Hake lab (HS) Zea mays cDNA, mRNA sequence.

ACCESSION AW076470

VERSION AW076470.1 GI:6031568

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 590)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 683018 row: G column: 06.

FEATURES Location/Qualifiers

source

1. .590
 /organism="Zea mays"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone_lib="683 - 14 day immature embryo from Hake lab (HS)"
 /tissue_type="embryo"
 /dev_stage="14 days after pollination"
 /lab_host="DH10B"
 /note="Organ: embryo; Vector: pBKCMV (Stratagene's Zap Express); Site_1: XhoI; Site_2: EcoRI; Directionally cloned, 14 day immature embryo library created with

Stratagene's Zap Express cDNA protocol."
BASE COUNT 123 a 172 c 156 g 139 t
ORIGIN

Query Match 69.8%; Score 291.8; DB 10; Length 590;
Best Local Similarity 82.7%; Pred. No. 5.8e-60;
Matches 345; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

```
Qy      2 gagagggaggggtcggcgcaggacatcgcaacaacggagccgaggcggtctgcaaaacc 61
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    570 GCGAAGGAGGGTTCGGCGCAGGACATCACGACGACGGAGCCACCGCAGCGCCTGCACAGCC 511

Qy     62 tgaccgtccgccccggcggttgccgtggactccatcgagttcacctacaccgacacaggtg 121
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    510 TCACCGTTCGTGCCAGTGCCGCGCTCGACTCCATCGAGTTCACGTATACTGACAGAGGTG 451

Qy    122 gccagacgcgcaccgctgggcgatgggggtggacttggcggcaacgtccggaagctcgatc 181
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    450 GCCAGAGGCGCGCCGCTGGGCGATGGGGTGGACTTGGCGGCAACCTTCGAACGATCGATC 391

Qy    182 ttggcgacgctgaatacgtcaaggaagtttctggaacgtacggcgcattcgaaggtgcga 241
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    390 TTGGCGACGCCGAGGATGTTCAGGGAGGTCTCAGGAACGTACGGCACATTTGAAGGAGCCA 331

Qy    242 ctaccctgacctcggttgaggattgtcaccagcaccgccagagcttggggggccatggggca 301
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    330 CCACGCTGACCTCGTTTCAGAATTCTCACCAGCA---GCAGGACATGGGGGCCATGGGGCG 274

Qy    302 tcnagagcgggacacgtttctgcatcanccggcaccatcggcagcagcatcgtgggattct 361
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    273 TCGAGAACGGGACGCGTTTCTGCATCACCGCGCCGGTCGGCAGCAGCATCGTGGGGTTCT 214

Qy    362 atggacgcgcgacgaacaggctcgtcgctgcgatcgggtgtctacctgcgccaacttt 418
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    213 ATGGACGCGCGACCAGCAGGCTCGTCGCTGCGCTTGGTGTTTACCTGCGCCGACTTT 157
```

RESULT 8
AW067268/c
LOCUS AW067268 587 bp mRNA EST 12-OCT-1999
DEFINITION 683021C02.x1 683 - 14 day immature embryo from Hake lab (HS) Zea
mays cDNA, mRNA sequence.
ACCESSION AW067268
VERSION AW067268.1 GI:6022340
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 587)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V

Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 683021 row: C column: 02.

FEATURES Location/Qualifiers
 source 1. .587
 /organism="Zea mays"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone_lib="683 - 14 day immature embryo from Hake lab (HS)"
 /tissue_type="embryo"
 /dev_stage="14 days after pollination"
 /lab_host="DH10B"
 /note="Organ: embryo; Vector: pBKCMV (Stratagene's Zap Express); Site_1: XhoI; Site_2: EcoRI; Directionally cloned, 14 day immature embryo library created with Stratagene's Zap Express cDNA protocol."
BASE COUNT 132 a 160 c 154 g 141 t
ORIGIN

Query Match 65.6%; Score 274; DB 10; Length 587;
Best Local Similarity 82.3%; Pred. No. 1e-55;
Matches 326; Conservative 0; Mismatches 67; Indels 3; Gaps 1;

```

Qy      23  acatcgcaacaacggagccgcccaggcgctctgcaaaacctgaccgtccgccccggcgcttg 82
        ||||| | | | ||||| || | || |||| | | | |||| | | | |||
Db      587  ACATCACGACGACGGAGCCACCGCAGCGCCTGCACAGCCTCACCGTTCGTGCCAGTGCCG 528

Qy      83  ccgtggactccatcgagttcacctacaccgacacaggtggccagacgcgcaccgctgggc 142
        ||||| ||||| ||||| ||||| || | || | ||||| ||||| ||||| ||||| |||||
Db      527  CCGTCGACTCCATCGAGTTCACGTATACTGACAGAGGTGGCCAGAGGCGCGCGCTGGGC 468

Qy     143  gatgggggtggacttggcgggaacgtccggaagctcgatcttggcgacgctgaatacgtca 202
        ||||| ||||| ||||| ||||| || | || | ||||| ||||| || | ||||
Db      467  GATGGGGTGGACTTGGCGGCAACCTTCGAACGATCGATCTTGGCGACGCCGAGGATGTCA 408

Qy     203  aggaagtttctggaacgtacggcgcatcgaaggtgcgactaccctgacctcgttgagga 262
        ||| || | | ||||| ||||| ||||| || | || | ||||| || | || |
Db      407  GGGAGGTCTCAGGAACGTACGGCACATTTGAAGGAGCCACCACGCTGACCTCGTTCAGAA 348

Qy     263  ttgtcaccagcaccgccagagcttgggggcatggggcatcnagagcgggacacgtttct 322
        || ||||| || | || | ||||| ||||| || | ||||| |||||
Db      347  TTCTCACCAGCA---GCAGGACATGGGGGCCATGGGGCGTCGAGAACGGGACGCGTTTCT 291

Qy     323  gcatcancggcaccatcggcagcagcatcgctgggattctatggacgcgcgacgaacaggc 382
        ||||| || | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      290  GCATCACCGCGCCGGTCGGCAGCAGCATCGTGGGGTTCTATGGACGCGCGACCAGCAGGC 231

Qy     383  tcgtcgctgcgatcggtgtctacctgcgccaaacttt 418
        ||||| ||||| ||||| ||||| |||||
Db      230  TCGTCGCTGCGCTTGGTGTTTACCTGCGCCGACTTT 195

```

RESULT 9
 AW181191/c
 LOCUS AW181191 525 bp mRNA EST 30-MAR-2000
 DEFINITION 687021F05.x1 687 - Early embryo from Delaware Zea mays cDNA, mRNA sequence.
 ACCESSION AW181191
 VERSION AW181191.1 GI:6448425
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 525)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 687021 row: F column: 05.
 FEATURES Location/Qualifiers
 source 1. .525
 /organism="Zea mays"
 /cultivar="Illinois High Oil"
 /db_xref="taxon:4577"
 /clone_lib="687 - Early embryo from Delaware"
 /tissue_type="embryo"
 /dev_stage="14, 21, 28, and 35 days after pollination"
 /lab_host="E. coli SOLR"
 /note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
 ; Site_2: EcoRI; Library was prepared by Statagene using
 the Uni-ZAP XR system (Stratagene BN937328-12). Clones
 were picked by a Q-bot after blue/white selection
 (ampicillin resistance - use 100 micrograms/microliter).
 Developed from a pool of equal amounts of RNA from
 developing embryos sampled at 14, 21, 28 and 35 days after
 pollination of the Illinois High Oil Maize Strain Cycle
 90. This closed strain has been selected for high oil
 concentration for 90 generations and originates from the
 1890s era open pollinated variety Burr's White"
 BASE COUNT 115 a 158 c 148 g 104 t
 ORIGIN

Query Match 64.7%; Score 270.4; DB 10; Length 525;
 Best Local Similarity 81.1%; Pred. No. 7.4e-55;
 Matches 326; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

Qy 14 cggcgcaggacatcgcaacaacggagccgccgaggcgtctgcaaaacctgaccgtccgcc 73
 ||| ||||| ||| || ||||| || || ||||| ||

[illegible]


```

/db_xref="taxon:4577"
/clone_lib="946 - tassel primordium prepared by Schmidt
lab"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="XLOLR"
/note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
Site_2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."

```

```

BASE COUNT      112 a      180 c      149 g      107 t
ORIGIN

```

```

Query Match          64.4%; Score 269.4; DB 10; Length 548;
Best Local Similarity 79.4%; Pred. No. 1.3e-54;
Matches 331; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

```

```

Qy      2 gagagggaggggtcggcgcaggacatcgcaacaacggagccgagggcgtctgcaaaacc 61
      || ||||| ||||| ||||| || || || || ||||| || || |
Db    487 GACCGGGAGGGTTCGGCACAGGACATCACGGCAGAGCGGCCACCGCAGCGTCTTCACAGCG 428

Qy     62 tgaccgtccgccccggcggttgccgtggactccatcgagttcacctacaccgacacaggtg 121
      | ||||| || | ||||| ||||| ||||| ||||| ||||| || || || || ||
Db    427 TCACCGTTCGTGCTGGCGTTGCCGTCGACTCCATCGAGTTCACCTATACTGACAGCGCTG 368

Qy    122 gccagacgcgcaccgctgggcgatggggtggacttggcgggcaacgtccggaagctcgatc 181
      | |||| | || | ||||| ||||| ||||| ||||| || || | || || |
Db    367 GGCAGAGGCGCGCCGCTGGGCGATGGGGTGGACTTGGCGGCAATGTTTGAACGATCGACC 308

Qy    182 ttggcgcagctgaatacgtcaaggaagtttctggaacgtacggcgcattcgaaggtgcga 241
      ||||| || || | |||| | |||| | |||| | |||| | |||| | |||| |
Db    307 TTGGCGACGCCGAGGATGTCAGGGAAGTCTCAGGAACATACGGCGCATTTGAAGGTGCCA 248

Qy    242 ctaccctgacctcggttgaggattgtcaccagcaccgccagagcttggggggccatggggca 301
      |||| | ||||| || | || | ||||| || | |||| | |||| | |||| |
Db    247 CTACGCTGACCTCGCTCAGGCTCGTCACCAGCA---GCAGAACCTGGGGCCCCTGGGGGG 191

Qy    302 tcnagagcgggacacggtttctgcatcanccggcaccatcggcagcagcatcgtgggattct 361
      || || | |||| | |||| | || | |||| | |||| | |||| | |||| |
Db    190 TCGAGAACGGGACGCGTTTCTCCGTCACGGCGCCCATCGGCAGCAGCATCGTGGGATTCT 131

Qy    362 atggacgcgcgcgaacaggtcgtcgctgcgatcgggtgtctacctgcgccaacttt 418
      ||| || || | ||||| || || ||||| || ||||| || |||| | || |
Db    130 ATGCGCGGGCGGGAACAGGCTCGTCGATGCTATCGGTGTTTACTTGCGTCAGATTT 74

```

```

RESULT 11
BE345799/c
LOCUS      BE345799      574 bp      mRNA                      EST          17-JUL-2000
DEFINITION 946026A06.y1 946 - tassel primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION  BE345799
VERSION    BE345799.1  GI:9255331
KEYWORDS   EST.

```


Qy 242 ctaccctgacctcggttgaggattgtcaccagcaccgccagagcttgggggcatggggca 301
 |||| |||||||| | ||| | |||||||| | ||| | |||| | ||||
 Db 327 CTACGCTGACCTCGCTCAGGCTCGTCACCAGCA---GCAGAACCTGGGGCCCCTGGGGGG 271

Qy 302 tcnagagcgggacacgtttctgcatcancggcaccatcggcagcagcatcgtgggattct 361
 || ||| |||||| |||||| | ||| | ||||||||||||||||||||
 Db 270 TCGAGAACGGGACGCGTTTCTCCGTCACGGCGCCCATCGGCAGCAGCATCGTGGGATTCT 211

Qy 362 atggacgcgcgacgaacaggctcgtcgctgcgatcgggtgtctacctgcgccaacttt 418
 ||| || ||| | |||||||| || |||||| || |||| || |||
 Db 210 ATGCGCGGGCGGGAACCAGGCTCGTCGATGCTATCGGTGTTTACTTGCGTCAGATTT 154

RESULT 12

BE510995/c

LOCUS BE510995 577 bp mRNA EST 07-AUG-2000
 DEFINITION 946057A08.x1 946 - tassel primordium prepared by Schmidt lab Zea
 mays cDNA, mRNA sequence.

ACCESSION BE510995

VERSION BE510995.1 GI:9732243

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 577)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946057 row: A column: 08.

FEATURES

source

Location/Qualifiers

1. .577

/organism="Zea mays"

/cultivar="OH43"

/db_xref="taxon:4577"

/clone_lib="946 - tassel primordium prepared by Schmidt
 lab"

/tissue_type="tassels"

/dev_stage="just after the transition from vegetative to
 inflorescence development"

/lab_host="XL0LR"

/note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
 Site_2: XhoI; George Chuck dissected immature tassels
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA
 library in HybriZAP. Sample insert size range was 350 bp
 to 3 Kb with a 1 Kb average."

BASE COUNT 120 a 187 c 157 g 113 t

ORIGIN

Query Match 64.4%; Score 269.4; DB 10; Length 577;
 Best Local Similarity 79.4%; Pred. No. 1.3e-54;
 Matches 331; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

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Qy      2 gagagggaggggtcggcgcaggacatcgcaacaacggagccgccgaggcgtctgcaaaacc 61
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Db    505 GACCGGGAGGGTCGGCACAGGACATCACGGCAGAGCGGCCACCGCAGCGTCTTCACAGCG 446

Qy     62 tgaccgtccgccccggcggttgccgtggactccatcgagttcacctacaccgacacaggtg 121
      | ||||| || || ||||| ||||| ||||| ||||| || || || || ||
Db    445 TCACCGTTTCGTGCTGGCGTTGCCGTCGACTCCATCGAGTTCACCTATACTGACAGCGCTG 386

Qy    122 gccagacgcgcaccgctgggcatgggggtggacttggcggcaacgtccggaagctcgatc 181
      | ||||| ||||| ||||| ||||| ||||| ||||| || || || || ||
Db    385 GGCAGAGGCGCGCCGCTGGGCGATGGGGTGGACTTGGCGGCAATGTTTGAACGATCGACC 326

Qy    182 ttggcgacgctgaatacgtcaaggaagtttctggaacgtacggcgcattcgaaggtgcga 241
      ||||| ||||| || || ||||| ||||| || ||||| ||||| ||||| ||
Db    325 TTGGCGACGCCGAGGATGTTCAGGGAAGTCTCAGGAACATACGGCGCATTTGAAGGTGCCA 266

Qy    242 ctaccctgacctcggttgaggattgtcaccagcaccgccagagcttggggggccatggggca 301
      ||||| ||||| || || || ||||| ||||| || || || || || || ||
Db    265 CTACGCTGACCTCGCTCAGGCTCGTCACCAGCA---GCAGAACCTGGGGCCCCTGGGGGG 209

Qy    302 tcnagagcgggacacgtttctgcatacncggcaccatcggcagcagcatcgtgggattct 361
      || || || ||||| ||||| || || || ||||| ||||| ||||| |||||
Db    208 TCGAGAACGGGACGCGTTTCTCCGTCACGGCGCCCATCGGCAGCAGCATCGTGGGATTCT 149

Qy    362 atggacgcgcgcgaacaggctcgctcgctgcgatcgggtgtctacctgcgccaacttt 418
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Db    148 ATGCGCGGGGCGGAACAGGCTCGTCGATGCTATCGGTGTTTACTTGCCTCAGATTT 92
  
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RESULT 13

AW498242/c
 LOCUS AW498242 579 bp mRNA EST 01-MAR-2000
 DEFINITION 660044H01.x2 660 - Mixed stages of anther and pollen Zea mays cDNA,
 mRNA sequence.
 ACCESSION AW498242
 VERSION AW498242.1 GI:7135742
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 579)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University

LOCUS AW519882 599 bp mRNA EST 06-MAR-2000
 DEFINITION 660054G12.y1 660 - Mixed stages of anther and pollen Zea mays cDNA, mRNA sequence.
 ACCESSION AW519882
 VERSION AW519882.1 GI:7162275
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 599)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 660054 row: G column: 12.
 FEATURES Location/Qualifiers
 source 1. 599
 /organism="Zea mays"
 /cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_lib="660 - Mixed stages of anther and pollen"
 /tissue_type="whole premieotic anthers to pollen shed"
 /dev_stage="premieotic anthers to pollen shed"
 /lab_host="XL0LR"
 /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI; Anther and pollen cDNA library. Directionally sequenced with 5' end at the EcoRI site. Created by Amie Franklin."
 BASE COUNT 118 a 162 c 193 g 126 t
 ORIGIN

Query Match 64.4%; Score 269.4; DB 10; Length 599;
 Best Local Similarity 79.4%; Pred. No. 1.3e-54;
 Matches 331; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

Qy 2 gagagggaggggtcggcgcaggacatcgcaacaacggagccgagggcgtctgcaaaacc 61
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 Db 91 GACCGGGAGGGTCGGCACAGGACATCACGGCAGAGCGGCCACCGCAGCGTCTTCACAGCG 150
 Qy 62 tgaccgtccgccccggcggttgccgtggactccatcgagttcacctacaccgacacaggtg 121
 | ||||| || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 151 TCACCGTTCGTGCTGGCGTTGCCGTCGACTCCATCGAGTTCACCTATACTGACAGCGCTG 210
 Qy 122 gccagacgcgcaccgctgggcgatggggtggacttggcggcaacgtccggaagctcgatc 181
 | |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 211 GGCAGAGGCGCGCCGCTGGGCGATGGGGTGGACTTGGCGGCAATGTTTGAACGATCGACC 270

Qy 182 ttggcgacgtgaatacgtcaaggaagtttctgg¹aacgtacggcgcatcgaaggtgcga 241
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 Db 271 TTGGCGACGCCGAGGATGTCAGGGAAGTCTCAGGAACATACGGCGCATTTGAAGGTGCCA 330

Qy 242 ctaccctgacctcggttgaggattgtcaccagcaccgccagagcttgggggcatggggca 301
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 Db 331 CTACGCTGACCTCGCTCAGGCTCGTCACCAGCA---GCAGAACCTGGGGCCCCTGGGGGG 387

Qy 302 tcnagagcgggacacgttttctgcatcancggcaccatcggcagcagcatcgtgggattct 361
 || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 388 TCGAGAACGGGACGCGTTTCTCCGTCACGGCGCCCATCGGCAGCAGCATCGTGGGATTCT 447

Qy 362 atggacgcgcgacgaacaggctcgtcgcgtgcgatcgggtgtctacctgcgccaacttt 418
 ||| || ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 448 ATGCGCGGGCGGGAACAGGCTCGTCGATGCTATCGGTGTTTACTTGCGTCAGATTT 504

RESULT 15

AW352698/c

LOCUS AW352698 577 bp mRNA EST 02-FEB-2000

DEFINITION 660034E10.x1 660 - Mixed stages of anther and pollen Zea mays cDNA, mRNA sequence.

ACCESSION AW352698

VERSION AW352698.1 GI:6851688

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 577)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
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 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 660034 row: E column: 10.

FEATURES Location/Qualifiers

source

1. .577
 /organism="Zea mays"
 /cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_lib="660 - Mixed stages of anther and pollen"
 /tissue_type="whole premieotic anthers to pollen shed"
 /dev_stage="premieotic anthers to pollen shed"
 /lab_host="XL0LR"
 /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI; Anther and pollen cDNA library. Directionally sequenced with 5' end at the EcoRI site. Created by Amie Franklin."

BASE COUNT 122 a 185 c 156 g 111 t 3 others

ORIGIN

Query Match 64.4%; Score 269; DB 10; Length 577;
 Best Local Similarity 79.1%; Pred. No. 1.6e-54;
 Matches 330; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

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Qy      2 gagagggaggggtcggcgcaggacatcgcaacaacggagccgcccaggcgtctgcaaaacc 61
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Db    512 GACCGGGAGGGTTCGGCACAGGACATCNCGGCAGAGCGGCCACCGCAGCGTCTTCACAGCG 453

Qy     62 tgaccgtccgccccggcggttgccgtggactccatcgagttcacctacaccgacacaggtg 121
      | |||| || | ||||| ||||| ||||| ||||| || || || || ||
Db    452 TCNCCGTTTCGTGCTGGCGTTGCCGTCGACTCCATCGAGTTCACCTATACTGACAGCGCTG 393

Qy    122 gccagacgcgcaccgctgggcgatggggtggacttggcggcaacgtccggaagctcgatc 181
      | |||| |||| ||||| ||||| ||||| ||||| || || || || ||
Db    392 GGCAGAGGCGCGCCGCTGGGCGATGGGGTGGACTTGGCGGCAATGTTTGAACGATCGACC 333

Qy    182 ttggcgacgctgaatacgtcaaggaagtttctggaacgtacggcgcattcgaaggtgcga 241
      ||||| || || | |||| ||||| || ||||| ||||| ||||| || ||
Db    332 TTGGCGACGCCGAGGATGTCAGGGAAGTCTCAGGAACATACGGCGCATTTGAAGGTGCCA 273

Qy    242 ctaccctgacctcggttgaggattgtcaccagcaccgcccagagcttggggggccatggggca 301
      |||| ||||| || || || ||||| || || || || || || || || ||
Db    272 CTACGCTGACCTCGCTCAGGCTCGTCACCAGCA---GCAGAACCTGGGGCCCCTGGGGGG 216

Qy    302 tcnagagcgggacacgtttctgcatacncggcaccatcggcagcagcatcgtgggattct 361
      || || || ||||| ||||| || || || ||||| ||||| ||||| || ||
Db    215 TCGAGAACGGGACGCGTTTCTCCGTCACGGCGCCCATCGGCAGCAGCATCGTGGGATTCT 156

Qy    362 atggacgcgcgacgaacaggctcgtcgctgcgatcgggtgtctacctgcgccaacttt 418
      ||| || || || | ||||| || || ||||| || || || || || ||
Db    155 ATGCGCGGGCGGGAACCAAGGCTCGTCGATGCTATCGGTGTTTACTTGCGTCAGATTT 99
  
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